

SEQUENCE LISTING

<110> ASAHI KASEI KOGYO KABUSHIKI KAISHA

<120> Novel Gene

<130> X12-1408

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<170> PatentIn Ver. 2.0

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<213> Homo sapiens

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35 40 45

Ala Gly Pro Pro Pro Pro Gly Phe Lys Ser Glu Phe Thr Gly Pro Gln
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Asn Thr Gly His Gly Ala Thr Ser Gly Phe Gly Ser Ala Phe Thr Gly
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Gln Gln Gly Tyr Glu Asn Ser Gly Pro Gly Phe Trp Thr Gly Leu Gly
85 90 95

Thr Gly Gly Ile Leu Gly Tyr Leu Phe Gly Ser Asn Arg Ala Ala Thr
100 105 110

Pro Phe Ser Asp Ser Trp Tyr Tyr Pro Ser Tyr Pro Pro Ser Tyr Pro
115 120 125

Gly Thr Trp Asn Arg Ala Tyr Ser Pro Leu His Gly Gly Ser Gly Ser
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Pro Pro Pro Tyr Ser Glu Tyr Pro Pro Phe Ser His Arg Tyr Gln Arg

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Phe Thr Asn Ser Ala Gly Pro Pro Pro Gly Phe Lys Ser Glu Phe

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Thr Gly Leu Gly Thr Gly Gly Ile Leu Gly Tyr Leu Phe Gly Ser Asn

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Arg Ala Ala Thr Pro Phe Ser Asp Ser Trp Tyr Tyr Pro Ser Tyr Pro

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Pro Ser Tyr Pro Gly Thr Trp Asn Arg Ala Tyr Ser Pro Leu His Gly

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Gly Ser Gly Ser Tyr Ser Val Cys Ser Asn Ser Asp Thr Lys Thr Arg

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Thr Ala Ser Gly Tyr Gly Gly Thr Arg Arg Arg

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Tyr Asp Arg Tyr Thr Thr Ser Arg Arg Leu Asp Pro Ile Pro Gln Leu
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Lys Cys Val Gly Gly Thr Ala Gly Cys Asp Ser Tyr Thr Pro Lys Val
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Ile Gln Cys Gln Asn Lys Gly Trp Asp Gly Tyr Asp Val Gln Trp Glu
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Cys Lys Thr Asp Leu Asp Ile Ala Tyr Lys Phe Gly Lys Thr Val Val
100 105 110

Ser Cys Glu Gly Tyr Glu Ser Ser Glu Asp Gln Tyr Val Leu Arg Gly
115 120 125

Ser Cys Gly Leu Glu Tyr Asn Leu Asp Tyr Thr Glu Leu Gly Leu Gln
130 135 140

Lys Leu Lys Glu Ser Gly Lys Gln His Gly Phe Ala Ser Phe Ser Asp
145 150 155 160

Tyr Tyr Tyr Lys Trp Ser Ser Ala Asp Ser Cys Asn Met Ser Gly Leu
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Ile Thr Ile Val Val Leu Leu Gly Ile Ala Phe Val Val Tyr Lys Leu
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Phe Leu Ser Asp Gly Gln Tyr Ser Pro Pro Pro Tyr Ser Glu Tyr Pro
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Pro Phe Ser His Arg Tyr Gln Arg Phe Thr Asn Ser Ala Gly Pro Pro
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Pro Pro Gly Phe Lys Ser Glu Phe Thr Gly Pro Gln Asn Thr Gly His
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Gly Ala Thr Ser Gly Phe Gly Ser Ala Phe Thr Gly Gln Gln Gly Tyr
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Glu Asn Ser Gly Pro Gly Phe Trp Thr Gly Leu Gly Thr Gly Gly Ile
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Leu Gly Tyr Leu Phe Gly Ser Asn Arg Ala Ala Thr Pro Phe Ser Asp
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Ser Trp Tyr Tyr Pro Ser Tyr Pro Pro Ser Tyr Pro Gly Thr Trp Asn
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Arg Ala Tyr Ser Pro Leu His Gly Gly Ser Gly Ser Tyr Ser Val Cys

8/546

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 Pro Asp Arg Met Leu Leu Arg Asp Val Lys Ala Leu Thr Leu His Tyr
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 Asp Arg Tyr Thr Thr Ser Arg Arg Leu Asp Pro Ile Pro Gln Leu Lys
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 Cys Val Gly Gly Thr Ala Gly Cys Asp Ser Tyr Thr Pro Lys Val Ile
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cag tgt cag aac aaa ggc tgg gat ggg tat gat gta cag tgg gaa tgt 405
 Gln Cys Gln Asn Lys Gly Trp Asp Gly Tyr Asp Val Gln Trp Glu Cys
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aag acg gac tta gat att gca tac aaa ttt gga aaa act gtg gtg agc 453
 Lys Thr Asp Leu Asp Ile Ala Tyr Lys Phe Gly Lys Thr Val Val Ser
 100 105 110

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Cys Gly Leu Glu Tyr Asn Leu Asp Tyr Thr Glu Leu Gly Leu Gln Lys
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 Tyr Tyr Lys Trp Ser Ser Ala Asp Ser Cys Asn Met Ser Gly Leu Ile
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Gly Leu Ile Ala Pro Gly Pro Thr Thr Ala Val Ser Tyr Met Ser Val
 35 40 45

Lys Cys Val Asp Ala Arg Lys Asn His His Lys Thr Lys Trp Phe Val
 50 55 60

Pro Trp Gly Pro Asn His Cys Asp Lys Ile Arg Asp Ile Glu Glu Ala
 65 70 75 80

Ile Pro Arg Glu Ile Glu Ala Asn Asp Ile Val Phe Ser Val His Ile
 85 90 95

Pro Leu Pro His Met Glu Met Ser Pro Trp Phe Gln Phe Met Leu Phe
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cccagaaagg aggcgaggaa ggaggagtg tgtgagagga gggagcaaaa agtcaccct 180

aaaacattta tticaaggag aaaagaaaaa gggggggcgc aaaa atg gct ggg gca 236

Met Ala Gly Ala

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Ile Ile Glu Asn Met Ser Thr Lys Lys Leu Cys Ile Val Gly Gly Ile

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Leu Leu Val Phe Gln Ile Ile Ala Phe Leu Val Gly Gly Leu Ile Ala

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 Asn His Cys Asp Lys Ile Arg Asp Ile Glu Glu Ala Ile Pro Arg Glu
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Gly Leu Ile Ala Pro Gly Pro Thr Thr Ala Val Ser Tyr Met Ser Val

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Lys Cys Val Asp Ala Arg Lys Asn His His Lys Thr Lys Trp Phe Val

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Pro Trp Gly Pro Asn His Cys Asp Lys Ile Arg Asp Ile Glu Glu Ala

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75

80

Ile Pro Arg Glu Ile Glu Ala Asn Asp Ile Val Phe Ser Val His Ile

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90

95

Pro Leu Pro His Met Glu Met Ser Pro Trp Phe Gln Phe Met Leu Phe

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Ile Leu Gln Leu Asp Ile Ala Phe Lys Leu Asn Asn Gln Ile Arg Glu

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Asn Ala Glu Val Ser Met Asp Val Ser Leu Ala Tyr Arg Asp Asp Ala

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Phe Ala Glu Trp Thr Glu Met Ala His Glu Arg Val Pro Arg Lys Leu

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160

Lys Cys Thr Phe Thr Ser Pro Lys Thr Pro Glu His Glu Gly Arg Tyr

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170

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Tyr Glu Cys Asp Val Leu Pro Tyr Ala Gln His Leu His His Tyr Gly

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185

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Val Val Leu Glu Glu Asp His His Asp Val Pro Thr Pro Ser Ala Ser

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Gly Lys Ser His Leu Cys Pro Trp Asp Phe His Asp Leu Tyr Gln Tyr

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Pro Ser Gly Met Val Phe His Arg Val

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aaaacattta tttcaaggag aaaagaaaaa gggggggcgc aaaa atg gct ggg gca 236

Met Ala Gly Ala

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Leu Leu Val Phe Gln Ile Ile Ala Phe Leu Val Gly Gly Leu Ile Ala

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cca ggg ccc aca acg gca gtg tcc tac atg tgc gtg aaa tgt gtg gat 380

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Ala Arg Lys Asn His His Lys Thr Lys Trp Phe Val Pro Trp Gly Pro

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Asn His Cys Asp Lys Ile Arg Asp Ile Glu Glu Ala Ile Pro Arg Glu

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Ile Glu Ala Asn Asp Ile Val Phe Ser Val His Ile Pro Leu Pro His
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Met Glu Met Ser Pro Trp Phe Gln Phe Met Leu Phe Ile Leu Gln Leu
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Ser Met Asp Val Ser Leu Ala Tyr Arg Asp Asp Ala Phe Ala Glu Trp
135 140 145

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150 155 160

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185 190 195

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Glu Asp His His Asp Val Pro Thr Pro Ser Ala Ser Gly Lys Ser His
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Val Phe His Arg Val
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Ala Ala Lys Asn Phe Glu Asp Val Arg Cys Lys Cys Ile Cys Pro Pro
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Tyr Lys Glu Asn Ser Gly His Ile Tyr Asn Lys Asn Ile Ser Gln Lys
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Asp Cys Asp Cys Leu His Val Val Glu Pro Met Pro Val Arg Gly Pro
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Asp Val Glu Ala Tyr Cys Leu Arg Cys Glu Cys Lys Tyr Glu Glu Arg
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Ser Ser Val Thr Ile Lys Val Thr Ile Ile Ile Tyr Leu Ser Ile Leu

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Gly Leu Leu Leu Tyr Met Val Tyr Leu Thr Leu Val Glu Pro Ile

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120

125

Leu Lys Arg Arg Leu Phe Gly His Ala Gln Leu Ile Gln Ser Asp Asp

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135

140

Asp Ile Gly Asp His Gln Pro Phe Ala Asn Ala His Asp Val Leu Ala

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150

155

160

Arg Ser Arg Ser Arg Ala Asn Val Leu Asn Lys Val Glu Tyr Ala Gln

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Met Ala Thr Leu Trp Gly Gly Leu Leu

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5

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tgt aaa tgt atc tgc cct ccc tat aaa gaa aat tct ggg cat att tat 256

Cys Lys Cys Ile Cys Pro Pro Tyr Lys Glu Asn Ser Gly His Ile Tyr

45

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aat aag aac ata tct cag aaa gat tgt gat tgc ctt cat gtt gtg gag 304

Asn Lys Asn Ile Ser Gln Lys Asp Cys Asp Cys Leu His Val Val Glu

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70

ccc atg cct gtg cgg ggg cct gat gta gaa gca tac tgt cta cgc tgt 352

Pro Met Pro Val Arg Gly Pro Asp Val Glu Ala Tyr Cys Leu Arg Cys

75

80

85

gaa tgc aaa tat gaa gaa aga agc tct gtc aca atc aag gtt acc att 400

Glu Cys Lys Tyr Glu Glu Arg Ser Ser Val Thr Ile Lys Val Thr Ile
 90 95 100 105

ata att tat ctc tcc att ttg ggc ctt cta ctt ctg tac atg gta tat 448
 Ile Ile Tyr Leu Ser Ile Leu Gly Leu Leu Leu Tyr Met Val Tyr
 110 115 120

ctt act ctg gtt gag ccc ata ctg aag agg cgc ctc ttt gga cat gca 496
 Leu Thr Leu Val Glu Pro Ile Leu Lys Arg Arg Leu Phe Gly His Ala
 125 130 135

cag ttg ata cag agt gat gat gat att ggg gat cac cag cct ttt gca 544
 Gln Leu Ile Gln Ser Asp Asp Asp Ile Gly Asp His Gln Pro Phe Ala
 140 145 150

aat gca cac gat gtg cta gcc cgc tcc cgc agt cga gcc aac gtg ctg 592
 Asn Ala His Asp Val Leu Ala Arg Ser Arg Ser Arg Ala Asn Val Leu
 155 160 165

aac aag gta gaa tat gca cag cag cgc tgg aag ctt caa gtc caa gag 640
 Asn Lys Val Glu Tyr Ala Gln Gln Arg Trp Lys Leu Gln Val Gln Glu
 170 175 180 185

cag cga aag tct gtc ttt gac cgg cat gtt gtc ctc agc taattgggaa 689
 Gln Arg Lys Ser Val Phe Asp Arg His Val Val Leu Ser
 190 195

ttgaattcaa ggtgactaga aagaaacagg cagacaactg gaaagaactg actgggtttt 749

gctgggttc attttaatac cttgttgatt tcaccaactg ttgctggaag attcaaaact 809

ggaagcaaaa acttgcttga ttttttttc ttgttaacgt aataatagag acatttttaa 869

aagcacacag ctcaaagta gccataagt cttttcctat ttgtgacttt tactaataaa 929

aataaatctg cctgtaaatt atcttgaagt cctttaccig gaacaagcac tctcttttc 989

accacatagi ttttaactga ctttcaagat aattttcagg gtttttgtg ttgttgtttt 1049

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tcaagtcact ttactaaaca aacttttga aatagacctt accttctatt ttcgagtctc 1169

atttatattt tgcagtgtag ccagcctcat caaagagctg acttactcat ttgacttttg 1229

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1498

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<211> 221

<212> PRT

<213> Homo sapiens

<400> 11

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20 25 30

Gln Ala Ala Gly Asp Ala Pro Pro Pro Tyr Ser Ser Ile Ser Ala Glu

35 40 45

Ser Ala Ala Tyr Phe Asp Tyr Lys Asp Glu Ser Gly Phe Pro Lys Pro

50 55 60

Pro Ser Tyr Asn Val Ala Thr Thr Leu Pro Ser Tyr Asp Glu Ala Glu

65 70 75 80

Arg Thr Lys Ala Glu Ala Thr Ile Pro Leu Val Pro Gly Arg Asp Glu

85 90 95

Asp Phe Val Gly Arg Asp Asp Phe Asp Asp Ala Asp Gln Leu Arg Ile

100 105 110

Gly Asn Asp Gly Ile Phe Met Leu Thr Phe Phe Met Ala Phe Leu Phe

115 120 125

Asn Trp Ile Gly Phe Phe Leu Ser Phe Cys Leu Thr Thr Ser Ala Ala

130

135

140

Gly Arg Tyr Gly Ala Ile Ser Gly Phe Gly Leu Ser Leu Ile Lys Trp

145

150

155

160

Ile Leu Ile Val Arg Phe Ser Thr Tyr Phe Pro Gly Tyr Phe Asp Gly

165

170

175

Gln Tyr Trp Leu Trp Trp Val Phe Leu Val Leu Gly Phe Leu Leu Phe

180

185

190

Leu Arg Gly Phe Ile Asn Tyr Ala Lys Val Arg Lys Met Pro Glu Thr

195

200

205

Phe Ser Asn Leu Pro Arg Thr Arg Val Leu Phe Ile Tyr

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215

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<211> 1864

<212> DNA

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<220>

<221> CDS

<222> (153).. (815)

<400> 12

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gctcgctctg ctccctgct gccggctgcg cc atg gcg ttg gcg ttg gcg gcg 173

Met Ala Leu Ala Leu Ala Ala

1

5

ctg gcg gcg gtc gag ccg gcc tgc gcc agc cgg tac cag cag ttg cag 221

Leu Ala Ala Val Glu Pro Ala Cys Gly Ser Arg Tyr Gln Gln Leu Gln

10

15

20

aat gaa gaa gag tct gga gaa cct gaa cag gct gca ggt gat gct cct 269

Asn Glu Glu Glu Ser Gly Glu Pro Glu Gln Ala Ala Gly Asp Ala Pro

25

30

35

cca cct tac agc agc att tct gca gag agc gca gca tat ttt gac tac 317

Pro Pro Tyr Ser Ser Ile Ser Ala Glu Ser Ala Ala Tyr Phe Asp Tyr

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45

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55

aag gat gag tct ggg ttt cca aag ccc cca tet tac aat gta gct aca 365

Lys Asp Glu Ser Gly Phe Pro Lys Pro Pro Ser Tyr Asn Val Ala Thr

60

65

70

aca ctg ccc agt tat gat gaa gcg gag agg acc aag gct gaa gct act 413

Thr Leu Pro Ser Tyr Asp Glu Ala Glu Arg Thr Lys Ala Glu Ala Thr

75

80

85

atc cct ttg gtt cct ggg aga gat gag gat ttt gtg ggt cgg gat gat 461

Ile Pro Leu Val Pro Gly Arg Asp Glu Asp Phe Val Gly Arg Asp Asp

90

95

100

ttt gat gat gct gac cag ctg agg ata gga aat gat ggg att ttc atg 509
 Phe Asp Asp Ala Asp Gln Leu Arg Ile Gly Asn Asp Gly Ile Phe Met
 105 110 115

tta act ttt ttc atg gca ttc ctc ttt aac tgg att ggg ttt ttc ctg 557
 Leu Thr Phe Phe Met Ala Phe Leu Phe Asn Trp Ile Gly Phe Phe Leu
 120 125 130 135

tct ttt tgc ctg acc act tca gct gca gga agg tat ggg gcc att tca 605
 Ser Phe Cys Leu Thr Thr Ser Ala Ala Gly Arg Tyr Gly Ala Ile Ser
 140 145 150

gga ttt ggt ctc tct cta att aaa tgg atc ctg att gtc agg ttt tcc 653
 Gly Phe Gly Leu Ser Leu Ile Lys Trp Ile Leu Ile Val Arg Phe Ser
 155 160 165

acc tat ttc cct gga tat ttt gat ggt cag tac tgg ctc tgg tgg gtc 701
 Thr Tyr Phe Pro Gly Tyr Phe Asp Gly Gln Tyr Trp Leu Trp Trp Val
 170 175 180

ttc ctt gtt tta ggc ttt ctc ctg ttt ctc aga gga ttt atc aat tat 749
 Phe Leu Val Leu Gly Phe Leu Leu Phe Leu Arg Gly Phe Ile Asn Tyr
 185 190 195

gca aaa gtt cgg aag atg cca gaa act ttc tca aat ctc ccc agg acc 797
 Ala Lys Val Arg Lys Met Pro Glu Thr Phe Ser Asn Leu Pro Arg Thr
 200 205 210 215

aga gtt ctc ttt att tat taaagatggt ttctggcaaa ggccttcctg 845

Arg Val Leu Phe Ile Tyr

220

catttatgaa ttctctctca agaagcaaga gaacacctgc aggaagtga tcaagatgca 905

gaacacagag gaataatcac ctgctttaaa aaaataaagt actgttgaaa agatcatttc 965

ttctctattg ttcttaggtg taaaatttta atagttaatg cagaattctg taatcattga 1025

atcattagtg gttaatgttt gaaaaagctc ttgcaatcaa gtctgtgatg tattaataat 1085

gccttatata ttgtttgtag tcattttaag tagcatgagc catgtccctg tagtcggtag 1145

ggggcagctt tgctttattc atctccatc tcaaaatgaa ctggaatta aatattglaa 1205

gatatgtata atgctggcca ttttaaagg gttttctcaa aagttaaact ttgctatga 1265

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agaaaccagt gggttataat gtagaatgat gtgctttctg cccaagtgtt aattcatctt 1805

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<210> 13

<211> 242

<212> PRT

<213> Homo sapiens

<400> 13

Met Asp His His Gln Pro Gly Thr Gly Arg Tyr Gln Val Leu Leu Asn
1 5 10 15

Glu Glu Asp Asn Ser Glu Ser Ser Ala Ile Glu Gln Pro Pro Thr Ser
20 25 30

Asn Pro Ala Pro Gln Ile Val Gln Ala Ala Ser Ser Ala Pro Ala Leu
35 40 45

Glu Thr Asp Ser Ser Pro Pro Pro Tyr Ser Ser Ile Thr Val Glu Val
50 55 60

Pro Thr Thr Ser Asp Thr Glu Val Tyr Gly Glu Phe Tyr Pro Val Pro
65 70 75 80

Pro Pro Tyr Ser Val Ala Thr Ser Leu Pro Thr Tyr Asp Glu Ala Glu
85 90 95

Lys Ala Lys Ala Ala Ala Met Ala Ala Ala Ala Glu Thr Ser Gln
100 105 110

Arg Ile Gln Glu Glu Glu Cys Pro Pro Arg Asp Asp Phe Ser Asp Ala
115 120 125

Asp Gln Leu Arg Val Gly Asn Asp Gly Ile Phe Met Leu Ala Phe Phe
130 135 140

Met Ala Phe Ile Phe Asn Trp Leu Gly Phe Cys Leu Ser Phe Cys Ile
145 150 155 160

Thr Asn Thr Ile Ala Gly Arg Tyr Gly Ala Ile Cys Gly Phe Gly Leu
165 170 175

Ser Leu Ile Lys Trp Ile Leu Ile Val Arg Phe Ser Asp Tyr Phe Thr
180 185 190

Gly Tyr Phe Asn Gly Gln Tyr Trp Leu Trp Trp Ile Phe Leu Val Leu
195 200 205

Gly Leu Leu Leu Phe Phe Arg Gly Phe Val Asn Tyr Leu Lys Val Arg
210 215 220

Asn Met Ser Glu Ser Met Ala Ala Ala His Arg Thr Arg Tyr Phe Phe
 225 230 235 240

Leu Leu

<210> 14

<211> 2324

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (13).. (738)

<400> 14

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Met Asp His His Gln Pro Gly Thr Gly Arg Tyr Gln Val

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ctt ctt aat gaa gag gat aac tca gaa tca tcg gct ata gag cag cca 99

Leu Leu Asn Glu Glu Asp Asn Ser Glu Ser Ser Ala Ile Glu Gln Pro

15

20

25

cct act tca aac cca gca ccg cag att gtg cag gct gcg tct tca gca 147

Pro Thr Ser Asn Pro Ala Pro Gln Ile Val Gln Ala Ala Ser Ser Ala

30

35

40

45

cca gca ctt gaa act gac tct tcc cct cca cca tat agt agt att act 195
Pro Ala Leu Glu Thr Asp Ser Ser Pro Pro Pro Tyr Ser Ser Ile Thr

50

55

60

gtg gaa gta cct aca act tca gat aca gaa gtt tac ggt gag ttt tat 243
Val Glu Val Pro Thr Thr Ser Asp Thr Glu Val Tyr Gly Glu Phe Tyr

65

70

75

ccc gtg cca cct ccc tat agc gtt gct acc tct ctt cct aca tac gat 291
Pro Val Pro Pro Pro Tyr Ser Val Ala Thr Ser Leu Pro Thr Tyr Asp

80

85

90

gaa gct gag aag gct aaa gct gct gca atg gca gct gca gca gca gaa 339
Glu Ala Glu Lys Ala Lys Ala Ala Met Ala Ala Ala Ala Glu

95

100

105

aca tct caa aga att cag gag gaa gag tgt cca cca aga gat gac ttc 387
Thr Ser Gln Arg Ile Gln Glu Glu Glu Cys Pro Pro Arg Asp Asp Phe

110

115

120

125

agt gat gca gac cag ctc aga gtg ggg aat gat ggc att ttc atg ctg 435
Ser Asp Ala Asp Gln Leu Arg Val Gly Asn Asp Gly Ile Phe Met Leu

130

135

140

gca ttt ttc atg gca ttt att ttc aac tgg ctt gga ttt tgt tta tcc 483
Ala Phe Phe Met Ala Phe Ile Phe Asn Trp Leu Gly Phe Cys Leu Ser

145

150

155

ttc tgt atc acc aat acc ata gct gga agg tat ggt gct atc tgc gga 531
Phe Cys Ile Thr Asn Thr Ile Ala Gly Arg Tyr Gly Ala Ile Cys Gly
160 165 170

ttt ggc ctt tcc ttg atc aaa tgg atc ctt att gtc agg ttt tct gat 579
Phe Gly Leu Ser Leu Ile Lys Trp Ile Leu Ile Val Arg Phe Ser Asp
175 180 185

tat ttt act gga tat ttc aat gga cag tat tgg ctt tgg tgg ata ttt 627
Tyr Phe Thr Gly Tyr Phe Asn Gly Gln Tyr Trp Leu Trp Trp Ile Phe
190 195 200 205

ctt gta ctt ggc ctg ctc ctt ttc ttc aga gga ttt gtt aat tat cta 675
Leu Val Leu Gly Leu Leu Leu Phe Phe Arg Gly Phe Val Asn Tyr Leu
210 215 220

aaa gtc aga aac atg tct gaa agt atg gca gct gct cat aga aca agg 723
Lys Val Arg Asn Met Ser Glu Ser Met Ala Ala Ala His Arg Thr Arg
225 230 235

tat ttc ttc tta ttg tagagactgc atcaaccga cattcctttc ttataccaat 778
Tyr Phe Phe Leu Leu
240

gtgaaatttc cagatcatct gtaaacctac aactttaata gaagactact aataacagaa 838

gacaaattag tgaagaaaag acggagtttc gaaattgaat ggcagggtgg tttttgctta 898

caagccattt ctgttcattc tttaagtatc tatatttcat ttgttttgca cataatgcata 958

tgigcccatt taagatattt gcatatactt gatagaaacc ataaagtigt agcagttaag 1018

tccagtcaca ttiggttaat cagtgtttga tataattgaa agagttgagt ggataaacag 1078

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actaatttta aattaagtga actaaatata tatgtgtata tgtatacaca tatatataca 1438

cacacacata tatatattta gaaacgtgag tgttaaagat agaatttgtt ttaggacaaa 1498

ttttaagaaa atgigggaat accaaaatgc ctttataaga aaaataaatt ttattttaag 1558

ggacatacta gttttaggga ttttcagatg ggaagctgca tttttaggat tgcccatctt 1618

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tcaaagttaa ttttctaat aagataattc tcatttgtgt ttgtctttta aaaggccaat 1738

aaaatactt tcagtatcat tgtaataatt ttttagagtt taatttgtaa agcttagcaa 1798

ataaaatctt gtactatgaa tagcttcttg ctttatgact ttaggattaa ctigtataaaa 1858

acatatcctg aactgagata tgcaaaatac tcattttcaa gttatggaaa tigtitttg 1918

gcatatagga ctgtggggtc tgtgtgtgta gtgagagtg gtagccacta ttataactgg 1978

aatttaatt acattcataa actactatat ttcccatctt gcaaatcatt ttatgtctca 2038

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<210> 15

<211> 242

<212> PRT

<213> Homo sapiens

<400> 15

Met Asp His His Gln Pro Gly Thr Gly Arg Tyr Gln Val Leu Leu Asn

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Glu Glu Asp Asn Ser Glu Ser Ser Ala Ile Glu Gln Pro Pro Thr Ser

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Asn Pro Ala Pro Gln Ile Val Gln Ala Val Ser Ser Ala Pro Ala Leu
35 40 45
Glu Thr Asp Ser Ser Pro Pro Pro Tyr Ser Ser Ile Thr Val Glu Val
50 55 60
Pro Thr Thr Ser Asp Thr Glu Val Tyr Gly Glu Phe Tyr Pro Val Pro
65 70 75 80
Pro Pro Tyr Ser Val Ala Thr Ser Leu Pro Thr Tyr Asp Glu Ala Glu
85 90 95
Lys Ala Lys Ala Ala Ala Met Ala Ala Ala Ala Glu Thr Ser Gln
100 105 110
Arg Ile Gln Glu Glu Glu Cys Pro Pro Arg Asp Asp Phe Ser Asp Ala
115 120 125
Asp Gln Leu Arg Val Gly Asn Asp Gly Ile Phe Met Leu Ala Phe Phe
130 135 140
Met Ala Phe Ile Phe Asn Trp Leu Gly Phe Cys Leu Ser Phe Cys Ile
145 150 155 160
Thr Asn Thr Ile Ala Gly Arg Tyr Gly Ala Ile Cys Gly Phe Gly Leu
165 170 175

Ser Leu Ile Lys Trp Ile Leu Ile Val Arg Phe Ser Asp Tyr Phe Thr
 180 185 190

Gly Tyr Phe Asn Gly Gln Tyr Trp Leu Trp Trp Ile Phe Leu Val Leu
 195 200 205

Gly Leu Leu Leu Phe Phe Arg Gly Phe Val Asn Tyr Leu Lys Val Arg
 210 215 220

Asn Met Ser Glu Ser Met Ala Ala Ala His Arg Thr Arg Tyr Phe Phe
 225 230 235 240

Leu Leu

<210> 16

<211> 2324

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (13).. (738)

<400> 16

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Met Asp His His Gln Pro Gly Thr Gly Arg Tyr Gln Val

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ctt ctt aat gaa gag gat aac tca gaa tca tgc gct ata gag cag cca 99
 Leu Leu Asn Glu Glu Asp Asn Ser Glu Ser Ser Ala Ile Glu Gln Pro

15

20

25

cct act tca aac cca gca ccg cag att gtg cag gct gtg tct tca gca 147
 Pro Thr Ser Asn Pro Ala Pro Gln Ile Val Gln Ala Val Ser Ser Ala

30

35

40

45

cca gca ctt gaa act gac tct tcc cct cca cca tat agt agt att act 195
 Pro Ala Leu Glu Thr Asp Ser Ser Pro Pro Pro Tyr Ser Ser Ile Thr

50

55

60

gtg gaa gta cct aca act tca gat aca gaa gtt tac ggt gag ttt tat 243
 Val Glu Val Pro Thr Thr Ser Asp Thr Glu Val Tyr Gly Glu Phe Tyr

65

70

75

ccc gtg cca cct ccc tat agc gtt gct acc tct ctt cct aca tac gat 291
 Pro Val Pro Pro Pro Tyr Ser Val Ala Thr Ser Leu Pro Thr Tyr Asp

80

85

90

gaa gct gag aag gct aaa gct gct gca atg gca gct gca gca gca gaa 339
 Glu Ala Glu Lys Ala Lys Ala Ala Ala Met Ala Ala Ala Ala Glu

95

100

105

aca tct caa aga att cag gag gaa gag tgt cca cca aga gat gac ttc 387
 Thr Ser Gln Arg Ile Gln Glu Glu Glu Cys Pro Pro Arg Asp Asp Phe

110

115

120

125

agt gat gca gac cag ctc aga gtg ggg aat gat ggc att ttc atg ctg 435
 Ser Asp Ala Asp Gln Leu Arg Val Gly Asn Asp Gly Ile Phe Met Leu

130

135

140

gca ttt ttc atg gca ttt att ttc aac tgg ctt gga ttt tgt tta tcc 483
 Ala Phe Phe Met Ala Phe Ile Phe Asn Trp Leu Gly Phe Cys Leu Ser

145

150

155

ttc tgt atc acc aat acc ata gct gga agg tat ggt gct atc tgc gga 531
 Phe Cys Ile Thr Asn Thr Ile Ala Gly Arg Tyr Gly Ala Ile Cys Gly

160

165

170

ttt ggc ctt tcc ttg atc aaa tgg atc ctt att gtc agg ttt tct gat 579
 Phe Gly Leu Ser Leu Ile Lys Trp Ile Leu Ile Val Arg Phe Ser Asp

175

180

185

tat ttt act gga tat ttc aat gga cag tat tgg ctt tgg tgg ata ttt 627
 Tyr Phe Thr Gly Tyr Phe Asn Gly Gln Tyr Trp Leu Trp Trp Ile Phe

190

195

200

205

ctt gta ctt ggc ctg ctc ctt ttc ttc aga gga ttt gtt aat tat cta 675
 Leu Val Leu Gly Leu Leu Leu Phe Phe Arg Gly Phe Val Asn Tyr Leu

210

215

220

aaa gtc aga aac atg tct gaa agt atg gca gct gct cat aga aca agg 723
 Lys Val Arg Asn Met Ser Glu Ser Met Ala Ala Ala His Arg Thr Arg

225

230

235

tat ttc ttc tta ttg tagagactgc atcaaccgga catcctttc ttataccaat 778

Tyr Phe Phe Leu Leu

240

gtgaaatttc cagatcatct gtaaacctac aactttaata gaagactact aataacagaa 838

gacaaattag tgaagaaaag acggagtctt gaaattgaat ggcagggtgg tttttgctta 898

caagccattt ctgttcattc ttttaaglatc tatatttcat ttgttttgca catatgcata 958

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actaatttta aattaagtga actaaatata tatgtgtata tgtatacaca tatatataca 1438

cacacacata tatatattta gaaacgtgag tgttaaagat agaatttggt ttaggacaaa 1498

ttttaagaaa atgtgggaat accaaatgtc ctttataaga aaaataaatt ttattttaag 1558

ggacatacta gttttaggga ttttcagatg ggaagctgca tttttaggat tgcccatctt 1618

aagagatctt gcaggaagag attgtattag atattatatt tttttcattt aagataattt 1678

tcaaagttaa ttttctaaat aagataattc tcatttgtgt ttgtctttta aaaggccaat 1738

aaaatatctt tcagtatcat tgaataaatt ttttagagtt taatttgtaa agcttagcaa 1798

ataaaaatctt gtactatgaa tagcttcttg ctttatgact ttaggattaa ctgttaaaaa 1858

acatatcctg aactgagata tgcaaaatac tcattttcaa gttatggaaa tgtgtttgtg 1918

gcatatagga ctgtggggtc tgtgtgtgta gtagagtggt gtagccacta ttataactgg 1978

aatttaattt acattcataa actactatat ttcccatctt gcaaatcatt ttatgtctca 2038

tctgtttttc ctttcggtta tatcttttgt ttgaatacc aacatttaaa atgatggat 2098

tttatctttt aaacttaaaa attatttaat acagctatat ggaccattata aaattgattt 2158

cttatttatt attagacatt actactaaaa ggtacatcta actattcagg gacatttttc 2218

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cattgtcttt gataaataaa acagttttgt ttigctaata tagcct 2324

<210> 17

<211> 336 .

<212> PRT

<213> Homo sapiens

<400> 17

Met Ala Arg Arg Arg Ser Gln Arg Val Cys Ala Ser Gly Pro Ser Met

1

5

10

15

Leu Asn Ser Ala Arg Gly Ala Pro Glu Leu Leu Arg Gly Thr Ala Thr

20

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Asn Ala Glu Val Ser Ala Ala Ala Ala Gly Ala Thr Gly Ser Glu Glu

35

40

45

Leu Pro Pro Gly Asp Arg Gly Cys Arg Asn Gly Gly Gly Arg Gly Pro

50

55

60

Ala Ala Thr Thr Ser Ser Thr Gly Val Ala Val Gly Ala Glu His Gly

65

70

75

80

Glu Asp Ser Leu Ser Arg Lys Pro Asp Pro Glu Pro Gly Arg Met Asp

85

90

95

His His Gln Pro Gly Thr Gly Arg Tyr Gln Val Leu Leu Asn Glu Glu

100

105

110

Asp Asn Ser Glu Ser Ser Ala Ile Glu Gln Pro Pro Thr Ser Asn Pro

115

120

125

Ala Pro Gln Ile Val Gln Ala Val Ser Ser Ala Pro Ala Leu Glu Thr

130 135 140
Asp Ser Ser Pro Pro Pro Tyr Ser Ser Ile Thr Val Glu Val Pro Thr
145 150 155 160
Thr Ser Asp Thr Glu Val Tyr Gly Glu Phe Tyr Pro Val Pro Pro Pro
165 170 175
Tyr Ser Val Ala Thr Ser Leu Pro Thr Tyr Asp Glu Ala Glu Lys Ala
180 185 190
Lys Ala Ala Ala Met Ala Ala Ala Ala Glu Thr Ser Gln Arg Ile
195 200 205
Gln Glu Glu Glu Cys Pro Pro Arg Asp Asp Phe Ser Asp Ala Asp Gln
210 215 220
Leu Arg Val Gly Asn Asp Gly Ile Phe Met Leu Ala Phe Phe Met Ala
225 230 235 240
Phe Ile Phe Asn Trp Leu Gly Phe Cys Leu Ser Phe Cys Ile Thr Asn
245 250 255
Thr Ile Ala Gly Arg Tyr Gly Ala Ile Cys Gly Phe Gly Leu Ser Leu
260 265 270
Ile Lys Trp Ile Leu Ile Val Arg Phe Ser Asp Tyr Phe Thr Gly Tyr
275 280 285

Phe Asn Gly Gln Tyr Trp Leu Trp Trp Ile Phe Leu Val Leu Gly Leu
 290 295 300

Leu Leu Phe Phe Arg Gly Phe Val Asn Tyr Leu Lys Val Arg Asn Met
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<213> Homo sapiens

<220>

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<222> (53).. (1060)

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 Arg Arg Arg Ser Gln Arg Val Cys Ala Ser Gly Pro Ser Met Leu Asn

5

10

15

agc gcg cgc ggc gcc ccg gag ctt ctc cgc gga acc gcg acc aac gcg 154

Ser Ala Arg Gly Ala Pro Glu Leu Leu Arg Gly Thr Ala Thr Asn Ala

20

25

30

gag gtc tcg gcg gcc gct gcg gga gcc aca gga agt gaa gag ctt ccg 202

Glu Val Ser Ala Ala Ala Gly Ala Thr Gly Ser Glu Glu Leu Pro

35

40

45

50

ccg gga gac cgc ggc tgc agg aac gga ggc gga agg ggc cct gcg gcg 250

Pro Gly Asp Arg Gly Cys Arg Asn Gly Gly Gly Arg Gly Pro Ala Ala

55

60

65

acg acg tcg tcg acg ggg gtg gcc gtg gga gct gag cac gga gaa gac 298

Thr Thr Ser Ser Thr Gly Val Ala Val Gly Ala Glu His Gly Glu Asp

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75

80

tcc ctc tct cgg aag ccg gat ccc gag ccg ggc agg atg gat cac cac 346

Ser Leu Ser Arg Lys Pro Asp Pro Glu Pro Gly Arg Met Asp His His

85

90

95

cag ccg ggg act ggg cgc tac cag gtg ctt ctt aat gaa gag gat aac 394

Gln Pro Gly Thr Gly Arg Tyr Gln Val Leu Leu Asn Glu Glu Asp Asn

100

105

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115

120

125

130

cag att gtg cag gct gtg tct tca gca cca gca ctt gaa act gac tct 490

Gln Ile Val Gln Ala Val Ser Ser Ala Pro Ala Leu Glu Thr Asp Ser

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Ser Pro Pro Pro Tyr Ser Ser Ile Thr Val Glu Val Pro Thr Thr Ser
150 155 160
gat aca gaa gtt tac ggt gag ttt tat ccc gtg cca cct ccc tat agc 586
Asp Thr Glu Val Tyr Gly Glu Phe Tyr Pro Val Pro Pro Pro Tyr Ser
165 170 175
gtt gct acc tct ctt cct aca tac gat gaa gct gag aag gct aaa gct 634
Val Ala Thr Ser Leu Pro Thr Tyr Asp Glu Ala Glu Lys Ala Lys Ala
180 185 190
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Ala Ala Met Ala Ala Ala Ala Glu Thr Ser Gln Arg Ile Gln Glu
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gaa gag tgt cca cca aga gat gac ttc agt gat gca gac cag ctc aga 730
Glu Glu Cys Pro Pro Arg Asp Asp Phe Ser Asp Ala Asp Gln Leu Arg
215 220 225
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Val Gly Asn Asp Gly Ile Phe Met Leu Ala Phe Phe Met Ala Phe Ile
230 235 240
ttc aac tgg ctt gga ttt tgt tta tcc ttc tgt atc acc aat acc ata 826
Phe Asn Trp Leu Gly Phe Cys Leu Ser Phe Cys Ile Thr Asn Thr Ile
245 250 255

gct gga agg tat ggt gct atc tgc gga ttt ggc ctt tcc ttg atc aaa 874
Ala Gly Arg Tyr Gly Ala Ile Cys Gly Phe Gly Leu Ser Leu Ile Lys

260

265

270

tgg atc ctt att gtc agg ttt tct gat tat ttt act gga tat ttc aat 922
Trp Ile Leu Ile Val Arg Phe Ser Asp Tyr Phe Thr Gly Tyr Phe Asn

275

280

285

290

gga cag tat tgg ctt tgg tgg ata ttt ctt gta ctt ggc ctg ctc ctt 970
Gly Gln Tyr Trp Leu Trp Trp Ile Phe Leu Val Leu Gly Leu Leu Leu

295

300

305

ttc ttc aga gga ttt gtt aat tat cta aaa gtc aga aac atg tct gaa 1018
Phe Phe Arg Gly Phe Val Asn Tyr Leu Lys Val Arg Asn Met Ser Glu

310

315

320

agt atg gca gct gct cat aga aca agg tat ttc ttc tta ttg 1060
Ser Met Ala Ala Ala His Arg Thr Arg Tyr Phe Phe Leu Leu

325

330

335

tagagactgc atcaaccga cattccttcc ttataccaat gtgaaatttc cagatcatct 1120

gtaaacctac aactttaata gaagactact aataacagaa gacaaattag tgaagaaaag 1180

acggagtctc gaaattgaat ggcagggtgg tttttgctta caagccattt ctgttcattc 1240

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actactaaaa ggtacatcta actattcagg gacatttttc catttccaaa aaataaaatt 2560

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2636

<210> 19

<211> 336

<212> PRT

<213> Homo sapiens

<400> 19

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Leu Asn Ser Ala Arg Gly Ala Pro Glu Leu Leu Arg Gly Thr Ala Thr

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25

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Asn Ala Glu Val Ser Ala Ala Ala Gly Ala Thr Gly Ser Glu Glu
35 40 45

Leu Pro Pro Gly Asp Arg Gly Cys Arg Asn Gly Gly Gly Arg Gly Pro
50 55 60

Ala Ala Thr Thr Ser Ser Thr Gly Val Ala Val Gly Ala Glu His Gly
65 70 75 80

Glu Asp Ser Leu Ser Arg Lys Pro Asp Pro Glu Pro Gly Arg Met Asp
85 90 95

His His Gln Pro Gly Thr Gly Arg Tyr Gln Val Leu Leu Asn Glu Glu
100 105 110

Asp Asn Ser Glu Ser Ser Ala Ile Glu Gln Pro Pro Thr Ser Asn Pro
115 120 125

Ala Pro Gln Ile Val Gln Ala Ala Ser Ser Ala Pro Ala Leu Glu Thr
130 135 140

Asp Ser Ser Pro Pro Pro Tyr Ser Ser Ile Thr Val Glu Val Pro Thr
145 150 155 160

Thr Ser Asp Thr Glu Val Tyr Gly Glu Phe Tyr Pro Val Pro Pro Pro
165 170 175

Tyr Ser Val Ala Thr Ser Leu Pro Thr Tyr Asp Glu Ala Glu Lys Ala

180 185 190
Lys Ala Ala Ala Met Ala Ala Ala Ala Glu Thr Ser Gln Arg Ile
195 200 205
Gln Glu Glu Glu Cys Pro Pro Arg Asp Asp Phe Ser Asp Ala Asp Gln
210 215 220
Leu Arg Val Gly Asn Asp Gly Ile Phe Met Leu Ala Phe Phe Met Ala
225 230 235 240
Phe Ile Phe Asn Trp Leu Gly Phe Cys Leu Ser Phe Cys Ile Thr Asn
245 250 255
Thr Ile Ala Gly Arg Tyr Gly Ala Ile Cys Gly Phe Gly Leu Ser Leu
260 265 270
Ile Lys Trp Ile Leu Ile Val Arg Phe Ser Asp Tyr Phe Thr Gly Tyr
275 280 285
Phe Asn Gly Gln Tyr Trp Leu Trp Trp Ile Phe Leu Val Leu Gly Leu
290 295 300
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Arg Arg Arg Ser Gln Arg Val Cys Ala Ser Gly Pro Ser Met Leu Asn

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15

agc gcg cgc ggc gcc ccg gag ctt ctc cgc gga acc gcg acc aac gcg 154

Ser Ala Arg Gly Ala Pro Glu Leu Leu Arg Gly Thr Ala Thr Asn Ala

20

25

30

gag gtc tcg gcg gcc gct gcg gga gcc aca gga agt gaa gag ctt ccg 202

Glu Val Ser Ala Ala Ala Ala Gly Ala Thr Gly Ser Glu Glu Leu Pro

35

40

45

50

ccg gga gac cgc ggc tgc agg aac gga ggc gga agg ggc cct gcg gcg 250

Pro Gly Asp Arg Gly Cys Arg Asn Gly Gly Gly Arg Gly Pro Ala Ala

55

60

65

acg acg tcg tcg acg ggg gtg gcc gtg gga gct gag cac gga gaa gac 298
 Thr Thr Ser Ser Thr Gly Val Ala Val Gly Ala Glu His Gly Glu Asp
 70 75 80

tcc ctc tct cgg aag ccg gat ccc gag ccg ggc agg atg gat cac cac 346
 Ser Leu Ser Arg Lys Pro Asp Pro Glu Pro Gly Arg Met Asp His His
 85 90 95

cag ccg ggg act ggg cgc tac cag gtg ctt ctt aat gaa gag gat aac 394
 Gln Pro Gly Thr Gly Arg Tyr Gln Val Leu Leu Asn Glu Glu Asp Asn
 100 105 110

tca gaa tca tcg gct ata gag cag cca cct act tca aac cca gca ccg 442
 Ser Glu Ser Ser Ala Ile Glu Gln Pro Pro Thr Ser Asn Pro Ala Pro
 115 120 125 130

cag att gtg cag gct gcg tct tca gca cca gca ctt gaa act gac tct 490
 Gln Ile Val Gln Ala Ala Ser Ser Ala Pro Ala Leu Glu Thr Asp Ser
 135 140 145

tcc cct cca cca tat agt agt att act gtg gaa gta cct aca act tca 538
 Ser Pro Pro Pro Tyr Ser Ser Ile Thr Val Glu Val Pro Thr Thr Ser
 150 155 160

gat aca gaa gtt tac ggt gag ttt tat ccc gtg cca cct ccc tat agc 586
 Asp Thr Glu Val Tyr Gly Glu Phe Tyr Pro Val Pro Pro Pro Tyr Ser
 165 170 175

ggt ggt acc tct ctt cct aca tac gat gaa gct gag aag gct aaa gct 634
 Val Ala Thr Ser Leu Pro Thr Tyr Asp Glu Ala Glu Lys Ala Lys Ala
 180 185 190

gct gca atg gca gct gca gca gca gaa aca tct caa aga att cag gag 682
 Ala Ala Met Ala Ala Ala Ala Glu Thr Ser Gln Arg Ile Gln Glu
 195 200 205 210

gaa gag tgt cca cca aga gat gac ttc agt gat gca gac cag ctc aga 730
 Glu Glu Cys Pro Pro Arg Asp Asp Phe Ser Asp Ala Asp Gln Leu Arg
 215 220 225

gtg ggg aat gat ggc att ttc atg ctg gca ttt ttc atg gca ttt att 778
 Val Gly Asn Asp Gly Ile Phe Met Leu Ala Phe Phe Met Ala Phe Ile
 230 235 240

ttc aac tgg ctt gga ttt tgt tta tcc ttc tgt atc acc aat acc ata 826
 Phe Asn Trp Leu Gly Phe Cys Leu Ser Phe Cys Ile Thr Asn Thr Ile
 245 250 255

gct gga agg tat ggt gct atc tgc gga ttt ggc ctt tcc ttg atc aaa 874
 Ala Gly Arg Tyr Gly Ala Ile Cys Gly Phe Gly Leu Ser Leu Ile Lys
 260 265 270

tgg atc ctt att gtc agg ttt tct gat tat ttt act gga tat ttc aat 922
 Trp Ile Leu Ile Val Arg Phe Ser Asp Tyr Phe Thr Gly Tyr Phe Asn
 275 280 285 290

gga cag tat tgg ctt tgg tgg ata ttt ctt gta ctt ggc ctg ctc ctt 970
 Gly Gln Tyr Trp Leu Trp Trp Ile Phe Leu Val Leu Gly Leu Leu Leu
 295 300 305

ttc ttc aga gga ttt gtt aat tat cta aaa gtc aga aac atg tct gaa 1018
 Phe Phe Arg Gly Phe Val Asn Tyr Leu Lys Val Arg Asn Met Ser Glu
 310 315 320

agt atg gca gct gct cat aga aca agg tat ttc ttc tta ttg 1060
 Ser Met Ala Ala Ala His Arg Thr Arg Tyr Phe Phe Leu Leu
 325 330 335

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2636

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<211> 76

<212> PRT

<213> Homo sapiens

<400> 21

Met Val Cys Ile Pro Cys Ile Val Ile Pro Val Leu Leu Trp Ile Tyr

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Lys Lys Phe Leu Glu Pro Tyr Ile Tyr Pro Leu Val Ser Pro Phe Val

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25

30

Ser Arg Ile Trp Pro Lys Lys Ala Ile Gln Glu Ser Asn Asp Thr Asn

35

40

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Lys Gly Lys Val Asn Phe Lys Gly Ala Asp Met Asn Gly Leu Pro Thr

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Lys Gly Pro Thr Glu Ile Cys Asp Lys Lys Lys Asp

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<210> 22

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<212> DNA

<213> Homo sapiens

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cgccctccgc ggtgcctgcc ttcgctctca ggttagaggag ctcaagcttg ggaaa atg 178

Met

1

gtg tgc att cct tgt atc gtc att cca gtt ctg ctc tgg atc tac aaa 226

Val Cys Ile Pro Cys Ile Val Ile Pro Val Leu Leu Trp Ile Tyr Lys

5

10

15

aaa ttc ctg gag cca tat ata tac cct ctg gtt tcc ccc ttc gtt agt 274

Lys Phe Leu Glu Pro Tyr Ile Tyr Pro Leu Val Ser Pro Phe Val Ser

20

25

30

cgt ata tgg cct aag aaa gca ata caa gaa tcc aat gat aca aac aaa 322

Arg Ile Trp Pro Lys Lys Ala Ile Gln Glu Ser Asn Asp Thr Asn Lys

35

40

45

ggc aaa gta aac ttt aag ggt gca gac atg aat gga tta cca aca aaa 370

Gly Lys Val Asn Phe Lys Gly Ala Asp Met Asn Gly Leu Pro Thr Lys

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55

60

65

gga cca aca gaa atc tgt gat aaa aag aaa gac taaagaaatt ttcctaaagg 423

Gly Pro Thr Glu Ile Cys Asp Lys Lys Lys Asp

70

75

accccatcat ttaaaaaatg gacctgataa tatgaagcat ctcccttgta attgtctctg 483

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1085

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<211> 84

<212> PRT

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Pro Glu Ile Gln Lys Pro Glu Arg Lys Ile Gln Phe Lys Glu Lys Val
20 25 30

Leu Trp Thr Ala Ile Thr Leu Phe Ile Phe Leu Val Cys Cys Gln Ile
35 40 45

Pro Leu Phe Gly Ile Met Ser Ser Asp Ser Ala Asp Pro Phe Tyr Trp
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Met Arg Val Ile Leu Ala Ser Asn Arg Gly Thr Leu Met Glu His Ser
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Leu Ser Gly Leu

<210> 24

<211> 1593

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (65).. (316)

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Met Ala Ile Lys Phe Leu Glu Val Ile Lys Pro Phe Cys Val Ile

1

5

10

15

ctg ccg gaa att cag aag cca gag agg aag att cag ttt aag gag aaa 157

Leu Pro Glu Ile Gln Lys Pro Glu Arg Lys Ile Gln Phe Lys Glu Lys

20

25

30

gtg ctg tgg acc gct atc acc ctc ttt atc ttc tta gtg tgc tgc cag 205

Val Leu Trp Thr Ala Ile Thr Leu Phe Ile Phe Leu Val Cys Cys Gln

35

40

45

att ccc ctg ttt ggg atc atg tct tca gat tca gct gac cct ttc tat 253

Ile Pro Leu Phe Gly Ile Met Ser Ser Asp Ser Ala Asp Pro Phe Tyr

50

55

60

tgg atg aga gtg att cta gcc tct aac aga ggc aca ttg atg gag cac 301
Trp Met Arg Val Ile Leu Ala Ser Asn Arg Gly Thr Leu Met Glu His
65 70 75

tct ctc tct ggc ctt tagggagtcc cctcttagga caggcactgc ccagcagcaa 356
Ser Leu Ser Gly Leu
80

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gcgtgcagcc tgcggggag accccactct gtgcacctat tggctcttct agctgactct 536

tctcgttggg cttagagtct gcctgtttct gctagctccg tgtttagtc accctgggtca 596

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<213> Homo sapiens

<400> 25

Met Ala Ile Lys Phe Leu Glu Val Ile Lys Pro Phe Cys Val Ile Leu
1 5 10 15

Pro Glu Ile Gln Lys Pro Glu Arg Lys Ile Gln Phe Lys Glu Lys Val
20 25 30

Leu Trp Thr Ala Ile Thr Leu Phe Ile Phe Leu Val Cys Cys Gln Ile
35 40 45

Pro Leu Phe Gly Ile Met Ser Ser Asp Ser Ala Asp Pro Val His Ala
50 55 60

Val Val Tyr Ile Val Phe Met Leu Gly Ser Cys Ala Phe Phe Ser Lys
65 70 75 80

Thr Trp Ile Glu Val Ser Gly Ser Ser Ala Lys Asp Val Ala Lys Gln
85 90 95

Leu Lys Glu Gln Gln Met Val Met Arg Gly His Arg Glu Thr Ser Met
100 105 110

Val His Glu Leu Asn Arg Tyr Ile Pro Thr Ala Ala Ala Phe Gly Gly
115 120 125

Leu Cys Ile Gly Ala Leu Ser Val Leu Ala Asp Phe Leu Gly Ala Ile
130 135 140

Gly Ser Gly Thr Gly Ile Leu Leu Ala Val Thr Ile Ile Tyr Gln Tyr

145

150

155

160

Phe Glu Ile Phe Val Lys Glu Gln Ser Glu Val Gly Ser Met Gly Ala

165

170

175

Leu Leu Phe

<210> 26

<211> 1820

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (114).. (650)

<400> 26

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acgcggagca gagctgagct gaagcgggac ccggagcccg agcagccgcc gcc atg 116

Met

1

gca atc aaa ttt ctg gaa gtc atc aag ccc ttc tgt gtc atc ctg ccg 164

Ala Ile Lys Phe Leu Glu Val Ile Lys Pro Phe Cys Val Ile Leu Pro

5

10

15

gaa att cag aag cca gag agg aag att cag ttt aag gag aaa gtg ctg 212
Glu Ile Gln Lys Pro Glu Arg Lys Ile Gln Phe Lys Glu Lys Val Leu

20

25

30

tgg acc gct atc acc ctc ttt atc ttc tta gtg tgc tgc cag att ccc 260
Trp Thr Ala Ile Thr Leu Phe Ile Phe Leu Val Cys Cys Gln Ile Pro

35

40

45

ctg ttt ggg atc atg tct tca gat tca gct gac ccg gtc cat gca gtt 308
Leu Phe Gly Ile Met Ser Ser Asp Ser Ala Asp Pro Val His Ala Val

50

55

60

65

gta tac ata gtg ttc atg ctg ggc tcc tgt gca ttc ttc tcc aaa acg 356
Val Tyr Ile Val Phe Met Leu Gly Ser Cys Ala Phe Phe Ser Lys Thr

70

75

80

tgg att gag gtc tca ggt tcc tct gcc aaa gat gtt gca aag cag ctg 404
Trp Ile Glu Val Ser Gly Ser Ser Ala Lys Asp Val Ala Lys Gln Leu

85

90

95

aag gag cag cag atg gtg atg aga ggc cac cga gag acc tcc atg gtc 452
Lys Glu Gln Gln Met Val Met Arg Gly His Arg Glu Thr Ser Met Val

100

105

110

cat gaa ctc aac cgg tac atc ccc aca gcc gcg gcc ttt ggt ggg ctg 500
His Glu Leu Asn Arg Tyr Ile Pro Thr Ala Ala Ala Phe Gly Gly Leu

115

120

125

tgc atc ggg gcc ctc tcg gtc ctg gct gac ttc cta ggc gcc att ggg 548

Cys Ile Gly Ala Leu Ser Val Leu Ala Asp Phe Leu Gly Ala Ile Gly
130 135 140 145

tct gga acc ggg atc ctg ctc gca gtc aca atc atc tac cag tac ttt 596
Ser Gly Thr Gly Ile Leu Leu Ala Val Thr Ile Ile Tyr Gln Tyr Phe
150 155 160

gag atc ttc gtt aag gag caa agc gag gtt ggc agc atg ggg gcc ctg 644
Glu Ile Phe Val Lys Glu Gln Ser Glu Val Gly Ser Met Gly Ala Leu
165 170 175

ctc ttc tgagcccgtc tcccggacag gttgaggaag ctgctccaga agcgccctcg 700
Leu Phe

aagggagct ctcacatg gcgctgctgc tgcggcatat ggacttttaa taatgtttt 760

gaatttcgta ttctttcatt ccactgtgta aagtgtaga cattttcaa tttaaaattt 820

tgccttttat cctggcactg gcaaaaagaa ctgtgaaagt gaatttatt agccgactgc 880

cagagaagtg ggaatggtat aggattgtcc ccaagtgtcc atgtaacttt tgttttaacc 940

tttgacatt ctacgtgctg tatgcggctg cagccgtctc acctgtttcc ccacaaagg 1000

aatttctcac tctggttga agcacaaca ctgaaatgac tacgtttcat ttggcagta 1060

gggtgtgaag ctgggagcag atcatgtatt tcccggagac atgggacctt gctggcatgt 1120

ctccttcaca atcaggcgig ggaatatctg gcttaggact gttctctct aagacacat 1180

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gaccaaggga caagaaggga ctgcctaaa gccaccacgc aactcagcag cagaaccaag 1360
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<210> 27

<211> 279

<212> PRT

<213> Homo sapiens

<400> 27

Met Glu Ala Val Val Asn Leu Tyr Gln Glu Val Met Lys His Ala Asp
1 5 10 15

Pro Arg Ile Gln Gly Tyr Pro Leu Met Gly Ser Pro Leu Leu Met Thr
20 25 30

Ser Ile Leu Leu Thr Tyr Val Tyr Phe Val Leu Ser Leu Gly Pro Arg
35 40 45

Ile Met Ala Asn Arg Lys Pro Phe Gln Leu Arg Gly Phe Met Ile Val
50 55 60

Tyr Asn Phe Ser Leu Val Ala Leu Ser Leu Tyr Ile Val Tyr Glu Phe
65 70 75 80

Leu Met Ser Gly Trp Leu Ser Thr Tyr Thr Trp Arg Cys Asp Pro Val
85 90 95

Asp Tyr Ser Asn Ser Pro Glu Ala Leu Arg Met Val Arg Val Ala Trp
100 105 110

Leu Phe Leu Phe Ser Lys Phe Ile Glu Leu Met Asp Thr Val Ile Phe
115 120 125

Ile Leu Arg Lys Lys Asp Gly Gln Val Thr Phe Leu His Val Phe His
130 135 140

His Ser Val Leu Pro Trp Ser Trp Trp Trp Gly Val Lys Ile Ala Pro

145

150

155

160

Gly Gly Met Gly Ser Phe His Ala Met Ile Asn Ser Ser Val His Val

165

170

175

Ile Met Tyr Leu Tyr Tyr Gly Leu Ser Ala Phe Gly Pro Val Ala Gln

180

185

190

Pro Tyr Leu Trp Trp Lys Lys His Met Thr Ala Ile Gln Leu Ile Gln

195

200

205

Phe Val Leu Val Ser Leu His Ile Ser Gln Tyr Tyr Phe Met Ser Ser

210

215

220

Cys Asn Tyr Gln Tyr Pro Val Ile Ile His Leu Ile Trp Met Tyr Gly

225

230

235

240

Thr Ile Phe Phe Met Leu Phe Ser Asn Phe Trp Tyr His Ser Tyr Thr

245

250

255

Lys Gly Lys Arg Leu Pro Arg Ala Leu Gln Gln Asn Gly Ala Pro Gly

260

265

270

Ile Ala Lys Val Lys Ala Asn

275

<210> 28

<211> 1472

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (119).. (955)

<400> 28

gcccagcaga tgaggaagtgcaggcaggc aggcctggccc cggggacttc tctctggccc 60

tgctccctcc gagcgctccg ccgttgccc cctggcccct acggagtcct tagccagg 118

atg gag gct gtt gtg aac ttg tac caa gag gtg atg aag cac gca gat 166
Met Glu Ala Val Val Asn Leu Tyr Gln Glu Val Met Lys His Ala Asp

1

5

10

15

ccc cgg atc cag ggc tac cct ctg atg ggg tcc ccc ttg cta atg acc 214
Pro Arg Ile Gln Gly Tyr Pro Leu Met Gly Ser Pro Leu Leu Met Thr

20

25

30

tcc att ctc ctg acc tac gtg tac ttc gtt ctc tca ctt ggg cct cgc 262
Ser Ile Leu Leu Thr Tyr Val Tyr Phe Val Leu Ser Leu Gly Pro Arg

35

40

45

atc atg gct aat cgg aag ccc ttc cag ctc cgt ggc ttc atg att gtc 310
Ile Met Ala Asn Arg Lys Pro Phe Gln Leu Arg Gly Phe Met Ile Val

50

55

60

tac aac ttc tca ctg gtg gca ctc tcc ctc tac att gtc tat gag ttc 358

Tyr Asn Phe Ser Leu Val Ala Leu Ser Leu Tyr Ile Val Tyr Glu Phe
65 70 75 80

ctg atg tcg ggc tgg ctg agc acc tat acc tgg cgc tgt gac cct gtg 406
Leu Met Ser Gly Trp Leu Ser Thr Tyr Thr Trp Arg Cys Asp Pro Val
85 90 95

gac tat tcc aac agc cct gag gca ctt agg atg gtt cgg gtg gcc tgg 454
Asp Tyr Ser Asn Ser Pro Glu Ala Leu Arg Met Val Arg Val Ala Trp
100 105 110

ctc ttc ctc ttc tcc aag ttc att gag ctg atg gac aca gtg atc ttt 502
Leu Phe Leu Phe Ser Lys Phe Ile Glu Leu Met Asp Thr Val Ile Phe
115 120 125

att ctc cga aag aaa gac ggg cag gtg acc ttc cta cat gtc ttc cat 550
Ile Leu Arg Lys Lys Asp Gly Gln Val Thr Phe Leu His Val Phe His
130 135 140

cac tct gtg ctt ccc tgg agc tgg tgg tgg ggg gta aag att gcc ccg 598
His Ser Val Leu Pro Trp Ser Trp Trp Trp Gly Val Lys Ile Ala Pro
145 150 155 160

gga gga atg ggc tct ttc cat gcc atg ata aac tct tcc gtg cat gtc 646
Gly Gly Met Gly Ser Phe His Ala Met Ile Asn Ser Ser Val His Val
165 170 175

ata atg tac ctg tac tac gga tta tct gcc ttt ggc cct gtg gca caa 694
Ile Met Tyr Leu Tyr Tyr Gly Leu Ser Ala Phe Gly Pro Val Ala Gln

180

185

190

ccc tac ctt tgg tgg aaa aag cac atg aca gcc att cag ctg atc cag 742
 Pro Tyr Leu Trp Trp Lys Lys His Met Thr Ala Ile Gln Leu Ile Gln
 195 200 205

ttt gtc ctg gtc tca ctg cac atc tcc cag tac tac ttt atg tcc agc 790
 Phe Val Leu Val Ser Leu His Ile Ser Gln Tyr Tyr Phe Met Ser Ser
 210 215 220

tgt aac tac cag tac cca gtc att att cac ctg atc tgg atg tat ggc 838
 Cys Asn Tyr Gln Tyr Pro Val Ile Ile His Leu Ile Trp Met Tyr Gly
 225 230 235 240

acc atc ttc ttc atg ctg ttc tcc aac ttc tgg tat cac tct tat acc 886
 Thr Ile Phe Phe Met Leu Phe Ser Asn Phe Trp Tyr His Ser Tyr Thr
 245 250 255

aag ggc aag cgg ctg ccc cgt gca ctt cag caa aat gga gct cca ggt 934
 Lys Gly Lys Arg Leu Pro Arg Ala Leu Gln Gln Asn Gly Ala Pro Gly
 260 265 270

att gcc aag gtc aag gcc aac tgagaagcat ggcctagata ggcgcccacc 985
 Ile Ala Lys Val Lys Ala Asn
 275

taagtgcctc aggactgcac cttagggcag tgtccgtcag tgcctctcc acctacacct 1045

gtgaccaagg cttatgtggt caggactgag caggggactg gccctcccct cccacagct 1105

gctctacagg gaccacggct ttggttcctc acccattcc cccgggcagc tccagggatg 1165

tggcctcatt gctgtctgcc actccagagc tgggggctaa aaggsgctga cagttatttc 1225

ccccccctg ccttaaaaact tgggagagga gcactcaggg ctggccccac aaagggcttc 1285

gtggcctttt tcttcacaca gaagaggtca gcaataatgt cactgtggac ccagtctcac 1345

tctccacccc cacacactga agcagtagct tctgggccaa aggtcagggc gggcgggggc 1405

ctgggaatac agcctgtgga ggctgcttac tcaacttggt tcttaattaa aagtacaga 1465

1472

ggaaacc

<210> 29

<211> 137

<212> PRT

<213> Homo sapiens

<400> 29

Met Gly Phe Gly Ala Thr Leu Ala Val Gly Leu Thr Ile Phe Val Leu

1

5

10

15

Ser Val Val Thr Ile Ile Ile Cys Phe Thr Cys Ser Cys Cys Cys Leu

20

25

30

Tyr Lys Thr Cys Arg Arg Pro Arg Pro Val Val Thr Thr Thr Thr Ser

35 40 45
 Thr Thr Val Val His Ala Pro Tyr Pro Gln Pro Pro Ser Val Pro Pro
 50 55 60
 Ser Tyr Pro Gly Pro Ser Tyr Gln Gly Tyr His Thr Met Pro Pro Gln
 65 70 75 80
 Pro Gly Met Pro Ala Ala Pro Tyr Pro Met Gln Tyr Pro Pro Pro Tyr
 85 90 95
 Pro Ala Gln Pro Met Gly Pro Pro Ala Tyr His Glu Thr Leu Ala Gly
 100 105 110
 Gly Ala Ala Ala Pro Tyr Pro Ala Ser Gln Pro Pro Tyr Asn Pro Ala
 115 120 125
 Tyr Met Asp Ala Pro Lys Ala Ala Leu
 130 135

<210> 30

<211> 1788

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (145).. (555)

<400> 30

gtgcttcctg tggcigacgt catctggagg agatttgctt tctttttctc caaaaggga 60

ggaaattgaa actgagtggc ccacgatggg aagaggggaa agcccagggg tacaggaggc 120

ctctgggtga aggcagaggc taac atg ggg ttc gga gcg acc ttg gcc gtt 171

Met Gly Phe Gly Ala Thr Leu Ala Val

1

5

ggc ctg acc atc ttt gtg ctg tct gtc gtc act atc atc atc tgc ttc 219

Gly Leu Thr Ile Phe Val Leu Ser Val Val Thr Ile Ile Ile Cys Phe

10

15

20

25

acc tgc tcc tgc tgc tgc ctt tac aag acg tgc cgc cga cca cgt ccg 267

Thr Cys Ser Cys Cys Cys Leu Tyr Lys Thr Cys Arg Arg Pro Arg Pro

30

35

40

gtt gtc acc acc acc aca tcc acc act gtg gtg cat gcc cct tat cct 315

Val Val Thr Thr Thr Thr Ser Thr Thr Val Val His Ala Pro Tyr Pro

45

50

55

cag cct cca agt gtg ccg ccc agc tac cct gga cca agc tac cag ggc 363

Gln Pro Pro Ser Val Pro Pro Ser Tyr Pro Gly Pro Ser Tyr Gln Gly

60

65

70

tac cac acc atg ccg cct cag cca ggg atg cca gca gca ccc tac cca 411

Tyr His Thr Met Pro Pro Gln Pro Gly Met Pro Ala Ala Pro Tyr Pro

75

80

85

atg cag tac cca cca cct tac cca gcc cag ccc atg gcc cca ccg gcc 459
Met Gln Tyr Pro Pro Pro Tyr Pro Ala Gln Pro Met Gly Pro Pro Ala

90

95

100

105

tac cac gag acc ctg gct gga gga gca gcc gcg ccc tac ccc gcc agc 507
Tyr His Glu Thr Leu Ala Gly Gly Ala Ala Ala Pro Tyr Pro Ala Ser

110

115

120

cag cct cct tac aac ccg gcc tac atg gat gcc ccg aag gcg gcc ctc 555
Gln Pro Pro Tyr Asn Pro Ala Tyr Met Asp Ala Pro Lys Ala Ala Leu

125

130

135

tgagcattcc ctggcctctc tggctgccac ttggttatgt tgtgtgtgtg cgtgagtgt 615

gtgcaggcgc ggctccttac gcccctatgt tgctgtgtgt gtccaggcac ggctccttac 675

gcccctatgt tgctgtgtgt gtccctgcctg tataatgtggc ttctctgat gctgacaagg 735

tggggaacaa tccttgccag agtgggctgg gaccagactt tgttctcttc ctcacctgaa 795

attatgcttc ctaaaatctc aagccaaact caaagaatgg ggtggtgggg ggcacctgt 855

gaggtggccc ctgagaggtg ggggcctctc cagggcacat ctggagtct tctccagctt 915

acctagggt gaccaagtag ggcctgtcac accagggtgg cgcagcttct tgtgtgatgc 975

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caagttggac ttgatcctt tgggcagatg tccattgct ccttgagcc tgcagcct 1155

gttggggatc aggcagctc ctgatgccag aacacctcag gcagagccct actcagctgt 1215

acctgtctgc ctggactgtc cctgtcccc gcattcccc tggaccagc tggagggcca 1275

catgcacaca cagcctagct gccccaggg agctctgtg ccttgcctgg cctgcccc 1335

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tgagtcctg ctcccgaca ccagcctcat ggaatatgca acaactcctg taccagtc 1575

cacgtgttc tggcagcagg gacacctggg ccaatgggc atctggacca aaggtgggt 1635

gtggggccct gcatggcagc tctggcccag acatgaatac ctcgtgttc tctccctct 1695

attactgttt caccagagct gtcttagctc aaatctgtt tgtttctgag tctagggtct 1755

gtacactgtt ttataataaa tgcaatcgtt tgg

1788

<210> 31

<211> 118

<212> PRT

<213> Homo sapiens

<400> 31

Met Gly Phe Gly Ala Thr Leu Ala Val Gly Leu Thr Ile Phe Val Leu

1

5

10

15

Ser Val Val Thr Ile Ile Ile Cys Phe Thr Cys Ser Cys Cys Cys Leu

20

25

30

Tyr Lys Thr Cys Arg Arg Pro Arg Pro Val Val Thr Thr Thr Thr Ser

35

40

45

Thr Thr Val Val His Ala Pro Tyr Pro Gln Pro Pro Ser Val Pro Pro

50

55

60

Ser Tyr Pro Gly Pro Ser Tyr Gln Gly Tyr His Thr Met Pro Pro Gln

65

70

75

80

Pro Gly Met Pro Ala Ala Pro Tyr Pro Met Gln Tyr Pro Pro Pro Tyr

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95

Pro Ala Gln Pro Met Gly Pro Pro Ala Tyr His Glu Thr Leu Ala Gly

100

105

110

Glu Cys Pro Cys Gln Leu

115

<210> 32

<211> 1908

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (91).. (444)

<400> 32

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ggaggcctct gggatgaaggc agaggctaac atg ggg ttc gga gcg acc ttg gcc 114
Met Gly Phe Gly Ala Thr Leu Ala

1

5

gtt ggc ctg acc atc ttt gtg ctg tct gtc gtc act atc atc atc tgc 162
Val Gly Leu Thr Ile Phe Val Leu Ser Val Val Thr Ile Ile Ile Cys

10

15

20

ttc acc tgc tcc tgc tgc tgc ctt tac aag acg tgc cgc cga cca cgt 210
Phe Thr Cys Ser Cys Cys Cys Leu Tyr Lys Thr Cys Arg Arg Pro Arg

25

30

35

40

ccg gtt gtc acc acc acc aca tcc acc act gtg gtg cat gcc cct tat 258
Pro Val Val Thr Thr Thr Thr Ser Thr Thr Val Val His Ala Pro Tyr

45

50

55

cct cag cct cca agt gtg ccg ccc agc tac cct gga cca agc tac cag 306

Pro Gln Pro Pro Ser Val Pro Pro Ser Tyr Pro Gly Pro Ser Tyr Gln
 60 65 70

ggc tac cac acc atg ccg cct cag cca ggg atg cca gca gca ccc tac 354
 Gly Tyr His Thr Met Pro Pro Gln Pro Gly Met Pro Ala Ala Pro Tyr
 75 80 85

cca atg cag tac cca cca cct tac cca gcc cag ccc atg ggc cca ccg 402
 Pro Met Gln Tyr Pro Pro Pro Tyr Pro Ala Gln Pro Met Gly Pro Pro
 90 95 100

gcc tac cac gag acc ctg gct ggt gag tgc ccc tgc caa ctc 444
 Ala Tyr His Glu Thr Leu Ala Gly Glu Cys Pro Cys Gln Leu
 105 110 115

tagccctgcc cgacttcccg agtctctgcc agcatccctc gggcacccat cccaaactac 504

atcactcaac aggcctctgc cctttctgc ttgctgcc ctcacacggc agcccacat 564

gctcacagcc aaccagggtc ctctctgctt tcaggaggag cagccgcgcc ctaccccgcc 624

agccagcctc cttaacaacc ggcctacatg gatgccccga aggcggccct ctgagcattc 684

cctggcctct ctggctgcc cttggttatg ttgtgtgtg gcgtgagtgg tgtgcaggcg 744

cggttcctta cgccccatgt gtgctgtgtg tgtccaggca cggttcctta cgccccatgt 804

gtgctgtgtg tgtcctgcct gtatatgtgg ctctctctga tgcagacaag gtggggaaca 864

atccttgcca gagtgggctg ggaccagact ttgttctctt cctcacctga aattatgctt 924

cctaaaaatct caagccaaac tcaaagaatg ggggtgggagg gggcaccttg tgaggtggcc 984

cctgagaggt gggggcctct ccagggcaca tctggagtgc tctccagct taccctaggg 1044

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cccctgggtt gtggaggga attggctcag agatggacaa cctggcaact gtgagtcctt 1644

gcttcccgac accagcctca tggaatatgc aacaactcct gtacccagct ccacggtgtt 1704

ctggcagcag ggacaccttg gccaatgggc catctggacc aaagtgggg tgtggggccc 1764

tggaaggcag ctctggccca gacatgaata cctcgtgttc ctctccctc tattactgtt 1824

tcaccagagc tgccttagct caaatctgtt gtgtttctga gtctagggtc tgtacacttg 1884

tttataataa atgcaatcgt ttgg

1908

<210> 33

<211> 168

<212> PRT

<213> Homo sapiens

<400> 33

Met Asn Ser Lys Gly Gln Tyr Pro Thr Gln Pro Thr Tyr Pro Val Gln

1

5

10

15

Pro Pro Gly Asn Pro Val Tyr Pro Gln Thr Leu His Leu Pro Gln Ala

20

25

30

Pro Pro Tyr Thr Asp Ala Pro Pro Ala Tyr Ser Glu Leu Tyr Arg Pro

35

40

45

Ser Phe Val His Pro Gly Ala Ala Thr Val Pro Thr Met Ser Ala Ala

50

55

60

Phe Pro Gly Ala Ser Leu Tyr Leu Pro Met Ala Gln Ser Val Ala Val

65

70

75

80

Gly Pro Leu Gly Ser Thr Ile Pro Met Ala Tyr Tyr Pro Val Gly Pro
 85 90 95

Ile Tyr Pro Pro Gly Ser Thr Val Leu Val Glu Gly Gly Tyr Asp Ala
 100 105 110

Gly Ala Arg Phe Gly Ala Gly Ala Thr Ala Gly Asn Ile Pro Pro Pro
 115 120 125

Pro Pro Gly Cys Pro Pro Asn Ala Ala Gln Leu Ala Val Met Gln Gly
 130 135 140

Ala Asn Val Leu Val Thr Gln Arg Lys Gly Asn Phe Phe Met Gly Gly
 145 150 155 160

Ser Asp Gly Gly Tyr Thr Ile Trp
 165

<210> 34

<211> 1897

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (70).. (573)

<400> 34

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gcaaccacc atg aac agc aaa ggt caa tat cca aca cag cca acc tac cct 111

Met Asn Ser Lys Gly Gln Tyr Pro Thr Gln Pro Thr Tyr Pro

1

5

10

gtg cag cct cct ggg aat cca gta tac cct cag acc ttg cat ctt cct 159

Val Gln Pro Pro Gly Asn Pro Val Tyr Pro Gln Thr Leu His Leu Pro

15

20

25

30

cag gct cca ccc tat acc gat gct cca cct gcc tac tca gag ctc tat 207

Gln Ala Pro Pro Tyr Thr Asp Ala Pro Pro Ala Tyr Ser Glu Leu Tyr

35

40

45

cgt ccg agc ttt gtg cac cca ggg gct gcc aca gtc ccc acc atg tca 255

Arg Pro Ser Phe Val His Pro Gly Ala Ala Thr Val Pro Thr Met Ser

50

55

60

gcc gca ttt cct gga gcc tct ctg tat ctt ccc atg gcc cag tct gtg 303

Ala Ala Phe Pro Gly Ala Ser Leu Tyr Leu Pro Met Ala Gln Ser Val

65

70

75

gct gtt ggg cct tta ggt tcc aca atc ccc atg gct tat tat cca gtc 351

Ala Val Gly Pro Leu Gly Ser Thr Ile Pro Met Ala Tyr Tyr Pro Val

80

85

90

ggt ccc atc tat cca cct ggc tcc aca gtg ctg gtg gaa gga ggg tat 399

Gly Pro Ile Tyr Pro Pro Gly Ser Thr Val Leu Val Glu Gly Gly Tyr

95

100

105

110

gat gca ggt gcc aga ttt gga gct ggg gct act gct ggc aac att cct 447
Asp Ala Gly Ala Arg Phe Gly Ala Gly Ala Thr Ala Gly Asn Ile Pro

115

120

125

cct cca cct cct gga tgc cct ccc aat gct gct cag ctt gca gtc atg 495
Pro Pro Pro Pro Gly Cys Pro Pro Asn Ala Ala Gln Leu Ala Val Met

130

135

140

cag gga gcc aac gtc ctc gta act cag cgg aag ggg aac ttc ttc atg 543
Gln Gly Ala Asn Val Leu Val Thr Gln Arg Lys Gly Asn Phe Phe Met

145

150

155

ggt ggt tca gat ggt ggc tac acc atc tgg tgaggaacca aggccacctc 593
Gly Gly Ser Asp Gly Gly Tyr Thr Ile Trp

160

165

tgtgccggga aagacatcac ataccttcag cacttctcac aatgtaactg ctttagtcat 653

attaacctga agttgcagtt tagacacatg ttgttgggt gtcttcttg tgcccaact 713

ttcaggcact tttaaattt aataaggaac catgtaatgg tagcagtacc tccctaaagc 773

attttgaggt aggggaggta tccattcata aatgaatgt ggtgaagcc gccctaagga 833

ttttccttta atttctctgg agtaatactg taccatactg gtctttgctt ttagtaataa 893

aacatcaaat taggtttgga gggaactttg atcttcttaa gaattaaagt tgccaaatta 953

ttctgattgg tctttaatct cctttaagtc ttgatatat attacttggt ataaatggaa 1013

cgcattagtt gtcigccttt tctttccat ccttgcccc acccaccca tctccaaccc 1073

tagtcttcca tticctcccg ccagtctcca ttgaatcaat ggtgcaggac agaaagccag 1133

tcagactaat ttctttcttt cctgcactt cccccactc gtcactttt aactagtgtt 1193

tcacaaggat cctctgaaac cctctctgtg cccaagtac agatgccatt acttctgctt 1253

tcgtatctcc tcaggcaaaa gttgaggggt ccttatgggc cctcctcata ggttgtctct 1313

gcatacacga acciaaccca aatttgcttt ggtgccagaa aaactgagct atgtttgaac 1373

aaagatgtcg tgcaaacgt actgtgaaca acagttggtt taaaatatga ggggcaagga 1433

ggaggatgca tticaaaagc ttgattgatg tgttcagagc taaattaaga ggagttttca 1493

gatcaaaaac tggttaccat tttttgtcag agtgtctgat gcggccactc attcggctcc 1553

ccagaattcc tagactgggt taatagggtc atatttgaa tgtctcacta caaatgact 1613

tgagtcaggt gaaatctcat tagggtttaa gaatatttca gggatcctta atgttttgat 1673

ttttgttttc tgaattgga ttttatttta ttttatctta taatttcagt tcatctaaat 1733

tgtgtgttct gtacatgtga tgtttgactg taccatigac tgttatggaa gttcagcgtt 1793

gtatgtctct cttacactg tggtcactt aacttggtga atttttatac taaaaatgta 1853

gaataaagac tatttgaag atttgaataa agtgatgaag ttgc

1897

<210> 35

<211> 455

<212> PRT

<213> Homo sapiens

<400> 35

Met Ser Phe Leu Ile Asp Ser Ser Ile Met Ile Thr Ser Gln Ile Leu
1 5 10 15

Phe Phe Gly Phe Gly Trp Leu Phe Phe Met Arg Gln Leu Phe Lys Asp
20 25 30

Tyr Glu Ile Arg Gln Tyr Val Val Gln Val Ile Phe Ser Val Thr Phe
35 40 45

Ala Phe Ser Cys Thr Met Phe Glu Leu Ile Ile Phe Glu Ile Leu Gly
50 55 60

Val Leu Asn Ser Ser Ser Arg Tyr Phe His Trp Lys Met Asn Leu Cys
65 70 75 80

Val Ile Leu Leu Ile Leu Val Phe Met Val Pro Phe Tyr Ile Gly Tyr
85 90 95

Phe Ile Val Ser Asn Ile Arg Leu Leu His Lys Gln Arg Leu Leu Phe

100 105 110
Ser Cys Leu Leu Trp Leu Thr Phe Met Tyr Phe Phe Trp Lys Leu Gly
115 120 125
Asp Pro Phe Pro Ile Leu Ser Pro Lys His Gly Ile Leu Ser Ile Glu
130 135 140
Gln Leu Ile Ser Arg Val Gly Val Ile Gly Val Thr Leu Met Ala Leu
145 150 155 160
Leu Ser Gly Phe Gly Ala Val Asn Cys Pro Tyr Thr Tyr Met Ser Tyr
165 170 175
Phe Leu Arg Asn Val Thr Asp Thr Asp Ile Leu Ala Leu Glu Arg Arg
180 185 190
Leu Leu Gln Thr Met Asp Met Ile Ile Ser Lys Lys Lys Arg Met Ala
195 200 205
Met Ala Arg Arg Thr Met Phe Gln Lys Gly Glu Val His Asn Lys Pro
210 215 220
Ser Gly Phe Trp Gly Met Ile Lys Ser Val Thr Thr Ser Ala Ser Gly
225 230 235 240
Ser Glu Asn Leu Thr Leu Ile Gln Gln Glu Val Asp Ala Leu Glu Glu
245 250 255

Leu Ser Arg Gln Leu Phe Leu Glu Thr Ala Asp Leu Tyr Ala Thr Lys
260 265 270

Glu Arg Ile Glu Tyr Ser Lys Thr Phe Lys Gly Lys Tyr Phe Asn Phe
275 280 285

Leu Gly Tyr Phe Phe Ser Ile Tyr Cys Val Trp Lys Ile Phe Met Ala
290 295 300

Thr Ile Asn Ile Val Phe Asp Arg Val Gly Lys Thr Asp Pro Val Thr
305 310 315 320

Arg Gly Ile Glu Ile Thr Val Asn Tyr Leu Gly Ile Gln Phe Asp Val
325 330 335

Lys Phe Trp Ser Gln His Ile Ser Phe Ile Leu Val Gly Ile Ile Ile
340 345 350

Val Thr Ser Ile Arg Gly Leu Leu Ile Thr Leu Thr Lys Phe Phe Tyr
355 360 365

Ala Ile Ser Ser Ser Lys Ser Ser Asn Val Ile Val Leu Leu Leu Ala
370 375 380

Gln Ile Met Gly Met Tyr Phe Val Ser Ser Val Leu Leu Ile Arg Met
385 390 395 400

Ser Met Pro Leu Glu Tyr Arg Thr Ile Ile Thr Glu Val Leu Gly Glu
405 410 415

Leu Gln Phe Asn Phe Tyr His Arg Trp Phe Asp Val Ile Phe Leu Val
 420 425 430

Ser Ala Leu Ser Ser Ile Leu Phe Leu Tyr Leu Ala His Lys Gln Ala
 435 440 445

Pro Glu Lys Gln Met Ala Pro
 450 455

<210> 36

<211> 1903

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (116).. (1480)

<400> 36

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tgctgtggcc tcgggagtg ggaagtggag gcaggagcct tccttacact tcgcc atg 118
 Met

1

agt ttc ctc atc gac tcc agc atc atg att acc tcc cag ata cta ttt 166
 Ser Phe Leu Ile Asp Ser Ser Ile Met Ile Thr Ser Gln Ile Leu Phe

5

10

15

ttt gga ttt ggg tgg ctt ttc ttc atg cgc caa ttg ttt aaa gac tat 214
 Phe Gly Phe Gly Trp Leu Phe Phe Met Arg Gln Leu Phe Lys Asp Tyr

20

25

30

gag ata cgt cag tat gtt gta cag gtg atc ttc tcc gtg acg ttt gca 262
 Glu Ile Arg Gln Tyr Val Val Gln Val Ile Phe Ser Val Thr Phe Ala

35

40

45

ttt tct tgc acc atg ttt gag ctc atc atc ttt gaa atc tta gga gta 310
 Phe Ser Cys Thr Met Phe Glu Leu Ile Ile Phe Glu Ile Leu Gly Val

50

55

60

65

ttg aat agc agc tcc cgt tat ttt cac tgg aaa atg aac ctg tgt gta 358
 Leu Asn Ser Ser Ser Arg Tyr Phe His Trp Lys Met Asn Leu Cys Val

70

75

80

att ctg ctg atc ctg gtt ttc atg gtg cct ttt tac att ggc tat ttt 406
 Ile Leu Leu Ile Leu Val Phe Met Val Pro Phe Tyr Ile Gly Tyr Phe

85

90

95

att gtg agc aat atc cga cta ctg cat aaa caa cga ctg ctt ttt tcc 454
 Ile Val Ser Asn Ile Arg Leu Leu His Lys Gln Arg Leu Leu Phe Ser

100

105

110

tgt ctc tta tgg ctg acc ttt atg tat ttc ttc tgg aaa cta gga gat 502
 Cys Leu Leu Trp Leu Thr Phe Met Tyr Phe Phe Trp Lys Leu Gly Asp

115

120

125

ccc ttt ccc att ctc agc cca aaa cat ggg atc tta tcc ata gaa cag 550
Pro Phe Pro Ile Leu Ser Pro Lys His Gly Ile Leu Ser Ile Glu Gln
130 135 140 145

ctc atc agc cgg gtt ggt gtg att gga gtg act ctc atg gct ctt ctt 598
Leu Ile Ser Arg Val Gly Val Ile Gly Val Thr Leu Met Ala Leu Leu
150 155 160

tct gga ttt ggt gct gtc aac tgc cca tac act tac atg tct tac ttc 646
Ser Gly Phe Gly Ala Val Asn Cys Pro Tyr Thr Tyr Met Ser Tyr Phe
165 170 175

ctc agg aat gtg act gac acg gat att cta gcc ctg gaa cgg cga ctg 694
Leu Arg Asn Val Thr Asp Thr Asp Ile Leu Ala Leu Glu Arg Arg Leu
180 185 190

ctg caa acc atg gat atg atc ata agc aaa aag aaa agg atg gca atg 742
Leu Gln Thr Met Asp Met Ile Ile Ser Lys Lys Lys Arg Met Ala Met
195 200 205

gca cgg aga aca atg ttc cag aag ggg gaa gtg cat aac aaa cca tca 790
Ala Arg Arg Thr Met Phe Gln Lys Gly Glu Val His Asn Lys Pro Ser
210 215 220 225

ggt ttc tgg gga atg ata aaa agt gtt acc act tca gca tca gga agt 838
Gly Phe Trp Gly Met Ile Lys Ser Val Thr Thr Ser Ala Ser Gly Ser
230 235 240

gaa aat ctt act ctt att caa cag gaa gtg gat gct ttg gaa gaa tta 886
 Glu Asn Leu Thr Leu Ile Gln Gln Glu Val Asp Ala Leu Glu Glu Leu
 245 250 255

agc agg cag ctt ttt ctg gaa aca gct gat cta tat gct acc aag gag 934
 Ser Arg Gln Leu Phe Leu Glu Thr Ala Asp Leu Tyr Ala Thr Lys Glu
 260 265 270

aga ata gaa tac tcc aaa acc ttc aag ggg aaa tat ttt aat ttt ctt 982
 Arg Ile Glu Tyr Ser Lys Thr Phe Lys Gly Lys Tyr Phe Asn Phe Leu
 275 280 285

ggt tac ttt ttc tct att tac tgt gtt tgg aaa att ttc atg gct acc 1030
 Gly Tyr Phe Phe Ser Ile Tyr Cys Val Trp Lys Ile Phe Met Ala Thr
 290 295 300 305

atc aat att gtt ttt gat cga gtt ggg aaa acg gat cct gtc aca aga 1078
 Ile Asn Ile Val Phe Asp Arg Val Gly Lys Thr Asp Pro Val Thr Arg
 310 315 320

ggc att gag atc act gtg aat tat ctg gga atc caa ttt gat gtg aag 1126
 Gly Ile Glu Ile Thr Val Asn Tyr Leu Gly Ile Gln Phe Asp Val Lys
 325 330 335

ttt tgg tcc caa cac att tcc ttc att ctt gtt gga ata atc atc gtc 1174
 Phe Trp Ser Gln His Ile Ser Phe Ile Leu Val Gly Ile Ile Ile Val
 340 345 350

aca tcc atc aga gga ttg ctg atc act ctt acc aag ttc ttt tat gcc 1222

Thr Ser Ile Arg Gly Leu Leu Ile Thr Leu Thr Lys Phe Phe Tyr Ala

355

360

365

atc tct agc agt aag tcc tcc aat gtc att gtc ctg cta tta gca cag 1270

Ile Ser Ser Ser Lys Ser Ser Asn Val Ile Val Leu Leu Leu Ala Gln

370

375

380

385

ata atg ggc atg tac ttt gtc tcc tct gtg ctg ctg atc cga atg agt 1318

Ile Met Gly Met Tyr Phe Val Ser Ser Val Leu Leu Ile Arg Met Ser

390

395

400

atg cct tta gaa tac cgc acc ata atc act gaa gtc ctt gga gaa ctg 1366

Met Pro Leu Glu Tyr Arg Thr Ile Ile Thr Glu Val Leu Gly Glu Leu

405

410

415

cag ttc aac ttc tat cac cgt tgg ttt gat gtg atc ttc ctg gtc agc 1414

Gln Phe Asn Phe Tyr His Arg Trp Phe Asp Val Ile Phe Leu Val Ser

420

425

430

gct ctc tct agc ata ctc ttc ctc tat ttg gct cac aaa cag gca cca 1462

Ala Leu Ser Ser Ile Leu Phe Leu Tyr Leu Ala His Lys Gln Ala Pro

435

440

445

gag aag caa atg gca cct tgaacttaag cctactacag actgttagag 1510

Glu Lys Gln Met Ala Pro

450

455

gccagtgggtt tcaaaattta gatataagag gggggaaaaa tggaaccagg gcctgacatt 1570

ttataaacaacaaaaatgct atggtagcat ttttcacctt catagcatat tccttccccg 1630
tcaggtgata ctatgaccat gagtagcatc agccagaaca tgagagggag aactaactca 1690
agacaatact cagcagagag catcccggtg ggatatgagg ctggtgtaga ggcggagagg 1750
agccaagaaa ctaaagggtga aaaatacact ggaactctgg ggcaagacat gtctatggta 1810
gctgagccaa acacgtagga tttccglttt aaggttcaca tggaaggt tatagcittg 1870
ccttgagatt gactcattaa aatcagagac tgt 1903

<210> 37

<211> 322

<212> PRT

<213> Homo sapiens

<400> 37

Met Ser Ser Leu Gly Gly Gly Ser Gln Asp Ala Gly Gly Ser Ser Ser
1 5 10 15

Ser Ser Thr Asn Gly Ser Gly Gly Ser Gly Ser Ser Gly Pro Lys Ala
20 25 30

Gly Ala Ala Asp Lys Ser Ala Val Val Ala Ala Ala Ala Pro Ala Ser
35 40 45

Val Ala Asp Asp Thr Pro Pro Pro Glu Arg Arg Asn Lys Ser Gly Ile

50

55

60

Ile Ser Glu Pro Leu Asn Lys Ser Leu Arg Arg Ser Arg Pro Leu Ser

65

70

75

80

His Tyr Ser Ser Phe Gly Ser Ser Gly Gly Ser Gly Gly Gly Ser Met

85

90

95

Met Gly Gly Glu Ser Ala Asp Lys Ala Thr Ala Ala Ala Ala Ala

100

105

110

Ser Leu Leu Ala Asn Gly His Asp Leu Ala Ala Ala Met Ala Val Asp

115

120

125

Lys Ser Asn Pro Thr Ser Lys His Lys Ser Gly Ala Val Ala Ser Leu

130

135

140

Leu Ser Lys Ala Glu Arg Ala Thr Glu Leu Ala Ala Glu Gly Gln Leu

145

150

155

160

Thr Leu Gln Gln Phe Ala Gln Ser Thr Glu Met Leu Lys Arg Val Val

165

170

175

Gln Glu His Leu Pro Leu Met Ser Glu Ala Gly Ala Gly Leu Pro Asp

180

185

190

Met Glu Ala Val Ala Gly Ala Glu Ala Leu Asn Gly Gln Ser Asp Phe

195

200

205

Pro Tyr Leu Gly Ala Phe Pro Ile Asn Pro Gly Leu Phe Ile Met Thr
210 215 220

Pro Ala Gly Val Phe Leu Ala Glu Ser Ala Leu His Met Ala Gly Leu
225 230 235 240

Ala Glu Tyr Pro Met Gln Gly Glu Leu Ala Ser Ala Ile Ser Ser Gly
245 250 255

Lys Lys Lys Arg Lys Arg Cys Gly Met Cys Ala Pro Cys Arg Arg Arg
260 265 270

Ile Asn Cys Glu Gln Cys Ser Ser Cys Arg Asn Arg Lys Thr Gly His
275 280 285

Gln Ile Cys Lys Phe Arg Lys Cys Glu Glu Leu Lys Lys Lys Pro Ser
290 295 300

Ala Ala Leu Glu Lys Val Met Leu Pro Thr Gly Ala Ala Phe Arg Trp
305 310 315 320

Phe Gln

<210> 38

<211> 1448

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (292).. (1257)

<400> 38

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ccctgccccg cccctcccc tggcctcgc ggcgacggcg gcggtggcgg ctggagcag 120

tcggagagcc gagtgaagac atttcacct ggacacctga ccatgtgcct gccctgagca 180

gcgaggccca ccaggcatct ctgttgigg cagcagggcc aggtcctgt ctgtggaccc 240

tcggcagttg gcaggctccc tctgcagtcg ggtctgggcc tcggccccac c atg tcg 297

Met Ser

1

agc ctc ggc ggt ggc tcc cag gat gcc ggc ggc agt agc agc agc agc 345

Ser Leu Gly Gly Gly Ser Gln Asp Ala Gly Gly Ser Ser Ser Ser Ser

5

10

15

acc aat ggc agc ggt ggc agt ggc agc agt ggc cca aag gca gga gca 393

Thr Asn Gly Ser Gly Gly Ser Gly Ser Ser Gly Pro Lys Ala Gly Ala

20

25

30

gca gac aag agt gca gtg gtg gct gcc gcc gca cca gcc tca gtg gca 441

Ala Asp Lys Ser Ala Val Val Ala Ala Ala Pro Ala Ser Val Ala

35

40

45

50

gat gac aca cca ccc ccc gag cgt cgg aac aag agc ggt atc atc agt 489
Asp Asp Thr Pro Pro Pro Glu Arg Arg Asn Lys Ser Gly Ile Ile Ser
55 60 65

gag ccc ctc aac aag agc ctg cgc cgc tcc cgc ccg ctc tcc cac tac 537
Glu Pro Leu Asn Lys Ser Leu Arg Arg Ser Arg Pro Leu Ser His Tyr
70 75 80

tct tct ttt ggc agc agt ggt ggt agt ggc ggt ggc agc atg atg ggc 585
Ser Ser Phe Gly Ser Ser Gly Gly Ser Gly Gly Gly Ser Met Met Gly
85 90 95

gga gag tct gct gac aag gcc act gcg gct gca gcc gct gcc tcc ctg 633
Gly Glu Ser Ala Asp Lys Ala Thr Ala Ala Ala Ala Ala Ser Leu
100 105 110

ttg gcc aat ggg cat gac ctg gcg gcg gcc atg gcg gtg gac aaa agc 681
Leu Ala Asn Gly His Asp Leu Ala Ala Ala Met Ala Val Asp Lys Ser
115 120 125 130

aac cct acc tca aag cac aaa agt ggt gct gtg gcc agc ctg ctg agc 729
Asn Pro Thr Ser Lys His Lys Ser Gly Ala Val Ala Ser Leu Leu Ser
135 140 145

aag gca gag cgg gcc acg gag ctg gca gcc gag gga cag ctg acg ctg 777
Lys Ala Glu Arg Ala Thr Glu Leu Ala Ala Glu Gly Gln Leu Thr Leu
150 155 160

cag cag ttt gcg cag tcc aca gag atg ctg aag cgc gtg gtg cag gag 825
Gln Gln Phe Ala Gln Ser Thr Glu Met Leu Lys Arg Val Val Gln Glu
165 170 175

cat ctc ccg ctg atg agc gag gcg ggt gct ggc ctg cct gac atg gag 873
His Leu Pro Leu Met Ser Glu Ala Gly Ala Gly Leu Pro Asp Met Glu
180 185 190

gct gtg gca ggt gcc gaa gcc ctc aat ggc cag tcc gac ttc ccc tac 921
Ala Val Ala Gly Ala Glu Ala Leu Asn Gly Gln Ser Asp Phe Pro Tyr
195 200 205 210

ctg ggc gct ttc ccc atc aac cca ggc ctc ttc att atg acc ccg gca 969
Leu Gly Ala Phe Pro Ile Asn Pro Gly Leu Phe Ile Met Thr Pro Ala
215 220 225

ggt gtg ttc ctg gcc gag agc gcg ctg cac atg gcg ggc ctg gct gag 1017
Gly Val Phe Leu Ala Glu Ser Ala Leu His Met Ala Gly Leu Ala Glu
230 235 240

tac ccc atg cag gga gag ctg gcc tct gcc atc agc tcc ggc aag aag 1065
Tyr Pro Met Gln Gly Glu Leu Ala Ser Ala Ile Ser Ser Gly Lys Lys
245 250 255

aag cgg aaa cgc tgc ggc atg tgc gcg ccc tgc cgg cgg cgc atc aac 1113
Lys Arg Lys Arg Cys Gly Met Cys Ala Pro Cys Arg Arg Arg Ile Asn
260 265 270

tgc gag cag tgc agc agt tgt agg aat cga aag act ggc cat cag att 1161

Cys Glu Gln Cys Ser Ser Cys Arg Asn Arg Lys Thr Gly His Gln Ile
 275 280 285 290

tgc aaa ttc aga aaa tgt gag gaa ctc aaa aag aag cct tcc gct gct 1209
 Cys Lys Phe Arg Lys Cys Glu Glu Leu Lys Lys Lys Pro Ser Ala Ala
 295 300 305

ctg gag aag gtg atg ctt ccg acg gga gcc gcc ttc cgg tgg ttt cag 1257
 Leu Glu Lys Val Met Leu Pro Thr Gly Ala Ala Phe Arg Trp Phe Gln
 310 315 320

tgacggcggc ggaacccaaa gctgccctct ccgtgcaatg tcactgctcg tgtggtctcc 1317

agcaagggat tcgggcgaag acaaacggat gcaccgtct ttagaaccaa aaatattctc 1377

tcacagattt cattcctgtt tttatatata tattttttgt tgtcgtttta acatctccac 1437

gtccctagca t

1448

<210> 39

<211> 313

<212> PRT

<213> Homo sapiens

<400> 39

Met Ala Gly Gln Pro Gly His Met Pro His Gly Gly Ser Ser Asn Asn

1

5

10

15

Leu Cys His Thr Leu Gly Pro Val His Pro Pro Asp Pro Gln Arg His
20 25 30

Pro Asn Thr Leu Ser Phe Arg Cys Ser Leu Ala Asp Phe Gln Ile Glu
35 40 45

Lys Lys Ile Gly Arg Gly Gln Phe Ser Glu Val Tyr Lys Ala Thr Cys
50 55 60

Leu Leu Asp Arg Lys Thr Val Ala Leu Lys Lys Val Gln Ile Phe Glu
65 70 75 80

Met Met Asp Ala Lys Ala Arg Gln Asp Cys Val Lys Glu Ile Gly Leu
85 90 95

Leu Lys Gln Leu Asn His Pro Asn Ile Ile Lys Tyr Leu Asp Ser Phe
100 105 110

Ile Glu Asp Asn Glu Leu Asn Ile Val Leu Glu Leu Ala Asp Ala Gly
115 120 125

Asp Leu Ser Gln Met Ile Lys Tyr Phe Lys Lys Gln Lys Arg Leu Ile
130 135 140

Pro Glu Arg Thr Val Trp Lys Tyr Phe Val Gln Leu Cys Ser Ala Val
145 150 155 160

Glu His Met His Ser Arg Arg Val Met His Arg Asp Ile Lys Pro Ala
165 170 175

Asn Val Phe Ile Thr Ala Thr Gly Val Val Lys Leu Gly Asp Leu Gly
180 185 190

Leu Gly Arg Phe Phe Ser Ser Glu Thr Thr Ala Ala His Ser Leu Val
195 200 205

Gly Thr Pro Tyr Tyr Met Ser Pro Glu Arg Ile His Glu Asn Gly Tyr
210 215 220

Asn Phe Lys Ser Asp Ile Trp Ser Leu Gly Cys Leu Leu Tyr Glu Met
225 230 235 240

Ala Ala Leu Gln Ser Pro Phe Tyr Gly Asp Lys Met Asn Leu Phe Ser
245 250 255

Leu Cys Gln Lys Ile Glu Gln Cys Asp Tyr Pro Pro Leu Pro Gly Glu
260 265 270

His Tyr Ser Glu Lys Leu Arg Glu Leu Val Ser Met Cys Ile Cys Pro
275 280 285

Asp Pro His Gln Arg Pro Asp Ile Gly Tyr Val His Gln Val Ala Lys
290 295 300

Gln Met His Ile Trp Met Ser Ser Thr
305 310

<210> 40

<211> 1597

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (153).. (1091)

<400> 40

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ctccagccgc ccgcggggcca gcgcaccggt cccccagcgg cagccgagcc cgcccgcgcg 120

ccgttcgtgc cctcgtgagg ctggcatgca gg atg gca gga cag ccc ggc cac 173

Met Ala Gly Gln Pro Gly His

1

5

atg ccc cat gga ggg agt tcc aac aac ctc tgc cac acc ctg ggg cct 221

Met Pro His Gly Gly Ser Ser Asn Asn Leu Cys His Thr Leu Gly Pro

10

15

20

gtg cat cct cct gac cca cag agg cat ccc aac acg ctg tct ttt cgc 269

Val His Pro Pro Asp Pro Gln Arg His Pro Asn Thr Leu Ser Phe Arg

25

30

35

tgc tgc ctg gcg gac ttc cag atc gaa aag aag ata ggc cga gga cag 317

Cys Ser Leu Ala Asp Phe Gln Ile Glu Lys Lys Ile Gly Arg Gly Gln

40

45

50

55

ttc agc gag gtg tac aag gcc acc tgc ctg ctg gac agg aag aca gtg 365
Phe Ser Glu Val Tyr Lys Ala Thr Cys Leu Leu Asp Arg Lys Thr Val

60

65

70

gct ctg aag aag gtg cag atc ttt gag atg atg gac gcc aag gcg agg 413
Ala Leu Lys Lys Val Gln Ile Phe Glu Met Met Asp Ala Lys Ala Arg

75

80

85

cag gac tgt gtc aag gag atc ggc ctc ttg aag caa ctg aac cac cca 461
Gln Asp Cys Val Lys Glu Ile Gly Leu Leu Lys Gln Leu Asn His Pro

90

95

100

aat atc atc aag tat ttg gac tgc ttt atc gaa gac aac gag ctg aac 509
Asn Ile Ile Lys Tyr Leu Asp Ser Phe Ile Glu Asp Asn Glu Leu Asn

105

110

115

att gtg ctg gag ttg gct gac gca ggg gac ctc tgc cag atg atc aag 557
Ile Val Leu Glu Leu Ala Asp Ala Gly Asp Leu Ser Gln Met Ile Lys

120

125

130

135

tac ttt aag aag cag aag cgg ctc atc ccg gag agg aca gta tgg aag 605
Tyr Phe Lys Lys Gln Lys Arg Leu Ile Pro Glu Arg Thr Val Trp Lys

140

145

150

tac ttt gtg cag ctg tgc agc gcc gtg gag cac atg cat tca cgc cgg 653
Tyr Phe Val Gln Leu Cys Ser Ala Val Glu His Met His Ser Arg Arg

155

160

165

gtg atg cac cga gac atc aag cct gcc aac gtg ttc atc aca gcc acg 701
Val Met His Arg Asp Ile Lys Pro Ala Asn Val Phe Ile Thr Ala Thr
170 175 180

ggc gtc gtg aag ctc ggt gac ctt ggt ctg ggc cgc ttc ttc agc tct 749
Gly Val Val Lys Leu Gly Asp Leu Gly Leu Gly Arg Phe Phe Ser Ser
185 190 195

gag acc acc gca gcc cac tcc cta gtg ggg acg ccc tac tac atg tca 797
Glu Thr Thr Ala Ala His Ser Leu Val Gly Thr Pro Tyr Tyr Met Ser
200 205 210 215

ccg gag agg atc cat gag aac ggc tac aac ttc aag tcc gac atc tgg 845
Pro Glu Arg Ile His Glu Asn Gly Tyr Asn Phe Lys Ser Asp Ile Trp
220 225 230

tcc ttg ggc tgt ctg ctg tac gag atg gca gcc ctc cag agc ccc ttc 893
Ser Leu Gly Cys Leu Leu Tyr Glu Met Ala Ala Leu Gln Ser Pro Phe
235 240 245

tat gga gat aag atg aat ctc ttc tcc ctg tgc cag aag atc gag cag 941
Tyr Gly Asp Lys Met Asn Leu Phe Ser Leu Cys Gln Lys Ile Glu Gln
250 255 260

tgt gac tac ccc cca ctc ccc ggg gag cac tac tcc gag aag tta cga 989
Cys Asp Tyr Pro Pro Leu Pro Gly Glu His Tyr Ser Glu Lys Leu Arg
265 270 275

gaa ctg gtc agc atg tgc atc tgc cct gac ccc cac cag aga cct gac 1037

Glu Leu Val Ser Met Cys Ile Cys Pro Asp Pro His Gln Arg Pro Asp
 280 285 290 295

atc gga tac gtg cac cag gtg gcc aag cag atg cac atc tgg atg tcc 1085
 Ile Gly Tyr Val His Gln Val Ala Lys Gln Met His Ile Trp Met Ser
 300 305 310

agc acc tgagcgtgga tgcaccgtgc cttatcaaag ccagcaccac ttgacctac 1141
 Ser Thr

ttgagtcgtc ttctcttcga gggccacct ggtagcctag aacagctaag accacagggt 1201

tcagcagggt ccccaaaagg ctgccagcc ttacagcaga tgctgaaggc agagcagctg 1261

aggaggggc gctggccaca tgtcactgat ggtcagattc caaagtcctt tctttatact 1321

gttgaggaca atctcagctg ggtaataag ggcagggtgt tcagcgagcc acggcagccc 1381

cctgtatctg gattglaatg tgaatcttta ggtaattcc tccagtgacc tgtcaaggct 1441

taigctaaca ggagacttgc aggagaccgt gtgatttgtg tagtgaccc ttgaaaatgg 1501

ttagtlaccgg gttcagttta gtcttttgta tcttttcaat caagctgtgt gcttaattta 1561

ctctgttgta aagggataaa ggggaaatca tttttt 1597

<210> 41

<211> 371

<212> PRT

<213> Homo sapiens

<400> 41

Met Ser His Glu Lys Ser Phe Leu Val Ser Gly Asp Asn Tyr Pro Pro

1

5

10

15

Pro Asn Pro Gly Tyr Pro Gly Gly Pro Gln Pro Pro Met Pro Pro Tyr

20

25

30

Ala Gln Pro Pro Tyr Pro Gly Ala Pro Tyr Pro Gln Pro Pro Phe Gln

35

40

45

Pro Ser Pro Tyr Gly Gln Pro Gly Tyr Pro His Gly Pro Ser Pro Tyr

50

55

60

Pro Gln Gly Gly Tyr Pro Gln Gly Pro Tyr Pro Gln Gly Gly Tyr Pro

65

70

75

80

Gln Gly Pro Tyr Pro Gln Glu Gly Tyr Pro Gln Gly Pro Tyr Pro Gln

85

90

95

Gly Gly Tyr Pro Gln Gly Pro Tyr Pro Gln Ser Pro Phe Pro Pro Asn

100

105

110

Pro Tyr Gly Gln Pro Gln Val Phe Pro Gly Gln Asp Pro Asp Ser Pro

115

120

125

Gln His Gly Asn Tyr Gln Glu Glu Gly Pro Pro Ser Tyr Tyr Asp Asn

130 135 140
Gln Asp Phe Pro Ala Thr Asn Trp Asp Asp Lys Ser Ile Arg Gln Ala
145 150 155 160
Phe Ile Arg Lys Val Phe Leu Val Leu Thr Leu Gln Leu Ser Val Thr
165 170 175
Leu Ser Thr Val Ser Val Phe Thr Phe Val Ala Glu Val Lys Gly Phe
180 185 190
Val Arg Glu Asn Val Trp Thr Tyr Tyr Val Ser Tyr Ala Val Phe Phe
195 200 205
Ile Ser Leu Ile Val Leu Ser Cys Cys Gly Asp Phe Arg Arg Lys His
210 215 220
Pro Trp Asn Leu Val Ala Leu Ser Val Leu Thr Ala Ser Leu Ser Tyr
225 230 235 240
Met Val Gly Met Ile Ala Ser Phe Tyr Asn Thr Glu Ala Val Ile Met
245 250 255
Ala Val Gly Ile Thr Thr Ala Val Cys Phe Thr Val Val Ile Phe Ser
260 265 270
Met Gln Thr Arg Tyr Asp Phe Thr Ser Cys Met Gly Val Leu Leu Val
275 280 285

Ser Met Val Val Leu Phe Ile Phe Ala Ile Leu Cys Ile Phe Ile Arg
290 295 300

Asn Arg Ile Leu Glu Ile Val Tyr Ala Ser Leu Gly Ala Leu Leu Phe
305 310 315 320

Thr Cys Phe Leu Ala Val Asp Thr Gln Leu Leu Leu Gly Asn Lys Gln
325 330 335

Leu Ser Leu Ser Pro Glu Glu Tyr Val Phe Ala Ala Leu Asn Leu Tyr
340 345 350

Thr Asp Ile Ile Asn Ile Phe Leu Tyr Ile Leu Thr Ile Ile Gly Arg
355 360 365

Ala Lys Glu
370

<210> 42

<211> 1781

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (91).. (1203)

<400> 42

attggccatc accgcgcggc cgcgcagcgg acaccgtgcg taccggccig cggcgcccgg 60

ccaccggggc ggaccgcgga acccgaggcc atg tcc cat gaa aag agt ttt ttg 114

Met Ser His Glu Lys Ser Phe Leu

1

5

gtg tct ggg gac aac tat cct ccc ccc aac cct gga tat ccg ggg ggg 162

Val Ser Gly Asp Asn Tyr Pro Pro Pro Asn Pro Gly Tyr Pro Gly Gly

10

15

20

ccc cag cca ccc atg ccc ccc tat gct cag cct ccc tac cct ggg gcc 210

Pro Gln Pro Pro Met Pro Pro Tyr Ala Gln Pro Pro Tyr Pro Gly Ala

25

30

35

40

cct tac cca cag ccc cct ttc cag ccc tcc ccc tac ggt cag cca ggg 258

Pro Tyr Pro Gln Pro Pro Phe Gln Pro Ser Pro Tyr Gly Gln Pro Gly

45

50

55

tac ccc cat ggc ccc agc ccc tac ccc caa ggg ggc tac cca cag ggt 306

Tyr Pro His Gly Pro Ser Pro Tyr Pro Gln Gly Gly Tyr Pro Gln Gly

60

65

70

ccc tac ccc caa ggg ggc tac cca cag ggc ccc tac cca caa gag ggc 354

Pro Tyr Pro Gln Gly Gly Tyr Pro Gln Gly Pro Tyr Pro Gln Glu Gly

75

80

85

tac cca cag ggc ccc tac ccc caa ggg ggc tac ccc cag ggg cca tat 402

Tyr Pro Gln Gly Pro Tyr Pro Gln Gly Gly Tyr Pro Gln Gly Pro Tyr

90

95

100

ccc cag agc ccc ttc ccc ccc aac ccc tat gga cag cca cag gtc ttc 450
Pro Gln Ser Pro Phe Pro Pro Asn Pro Tyr Gly Gln Pro Gln Val Phe
105 110 115 120

cca gga caa gac cct gac tca ccc cag cat gga aac tac cag gag gag 498
Pro Gly Gln Asp Pro Asp Ser Pro Gln His Gly Asn Tyr Gln Glu Glu
125 130 135

ggt ccc cca tcc tac tat gac aac cag gac ttc cct gcc acc aac tgg 546
Gly Pro Pro Ser Tyr Tyr Asp Asn Gln Asp Phe Pro Ala Thr Asn Trp
140 145 150

gat gac aag agc atc cga cag gcc ttc atc cgc aag gtg ttc cta gtg 594
Asp Asp Lys Ser Ile Arg Gln Ala Phe Ile Arg Lys Val Phe Leu Val
155 160 165

ctg acc ttg cag ctg tgg gtg acc ctg tcc acg gtg tct gtg ttc act 642
Leu Thr Leu Gln Leu Ser Val Thr Leu Ser Thr Val Ser Val Phe Thr
170 175 180

ttt gtt gcg gag gtg aag ggc ttt gtc cgg gag aat gtc tgg acc tac 690
Phe Val Ala Glu Val Lys Gly Phe Val Arg Glu Asn Val Trp Thr Tyr
185 190 195 200

tat gtc tcc tat gct gtc ttc ttc atc tct ctc atc gtc ctc agc tgt 738
Tyr Val Ser Tyr Ala Val Phe Phe Ile Ser Leu Ile Val Leu Ser Cys
205 210 215

tgt ggg gac ttc cgg cga aag cac ccc tgg aac ctt gtt gca ctg tgc 786
Cys Gly Asp Phe Arg Arg Lys His Pro Trp Asn Leu Val Ala Leu Ser
220 225 230

gtc ctg acc gcc agc ctg tgc tac atg gtg ggg atg atc gcc agc ttc 834
Val Leu Thr Ala Ser Leu Ser Tyr Met Val Gly Met Ile Ala Ser Phe
235 240 245

tac aac acc gag gca gtc atc atg gcc gtg ggc atc acc aca gcc gtc 882
Tyr Asn Thr Glu Ala Val Ile Met Ala Val Gly Ile Thr Thr Ala Val
250 255 260

tgc ttc acc gtc gtc atc ttc tcc atg cag acc cgc tac gac ttc acc 930
Cys Phe Thr Val Val Ile Phe Ser Met Gln Thr Arg Tyr Asp Phe Thr
265 270 275 280

tca tgc atg ggc gtg ctc ctg gtg agc atg gtg gtg ctc ttc atc ttc 978
Ser Cys Met Gly Val Leu Leu Val Ser Met Val Val Leu Phe Ile Phe
285 290 295

gcc att ctc tgc atc ttc atc cgg aac cgc atc ctg gag atc gtg tac 1026
Ala Ile Leu Cys Ile Phe Ile Arg Asn Arg Ile Leu Glu Ile Val Tyr
300 305 310

gcc tca ctg ggc gct ctg ctc ttc acc tgc ttc ctc gca gtg gac acc 1074
Ala Ser Leu Gly Ala Leu Leu Phe Thr Cys Phe Leu Ala Val Asp Thr
315 320 325

cag ctg ctg ctg ggg aac aag cag ctg tcc ctg agc cca gaa gag tat 1122

Gln Leu Leu Leu Gly Asn Lys Gln Leu Ser Leu Ser Pro Glu Glu Tyr
 330 335 340

gtg ttt gct gcg ctg aac ctg tac aca gac atc atc aac atc ttc ctg 1170
 Val Phe Ala Ala Leu Asn Leu Tyr Thr Asp Ile Ile Asn Ile Phe Leu
 345 350 355 360

tac atc ctc acc atc att ggc cgc gcc aag gag tagccgagct ccagctcgct 1223
 Tyr Ile Leu Thr Ile Ile Gly Arg Ala Lys Glu
 365 370

gtgcccgctc aggtggcacg gctggcctgg accctgcccc tggcacggca gtgccagctg 1283

tacttccct ctcctttgtc cccaggcaca gcctagggaa aaggatgcct ctcaccaacc 1343

ctcctgtatg tacactgcag atacttccat ttggaccgc tgiggccaca gcatggcccc 1403

tttagtcctc cgcggccgc caaggggcag caaggccag tttccgtgcc acctcctgtc 1463

tactcattgt tgcattgagc ctgtctgcca gccacccca gggactgggg gcagcaccag 1523

gtcccgggga gagggattga gccaaagggt gagggcgac gtcttcctc ctgtccagc 1583

tccccagct ggcgtagagc accctcccc tccccccac cccctggag tgctgccctc 1643

tggggacatg cggagtgggg gtcttatccc tgtgtgagc cctgaggga gagaggatgg 1703

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1781

tgggatttgc tctctgcc

<210> 43

<211> 393

<212> PRT

<213> Homo sapiens

<400> 43

Met Ser Asp Glu Arg Glu Val Ala Glu Ala Ala Thr Gly Glu Asp Ala

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10

15

Ser Ser Pro Pro Pro Lys Thr Glu Ala Ala Ser Asp Pro Gln His Pro

20

25

30

Ala Ala Ser Glu Gly Ala Ala Ala Ala Ala Ser Pro Pro Leu Leu

35

40

45

Arg Cys Leu Val Leu Thr Gly Phe Gly Gly Tyr Asp Lys Val Lys Leu

50

55

60

Gln Ser Arg Pro Ala Ala Pro Pro Ala Pro Gly Pro Gly Gln Leu Thr

65

70

75

80

Leu Arg Leu Arg Ala Cys Gly Leu Asn Phe Ala Asp Leu Met Ala Arg

85

90

95

Gln Gly Leu Tyr Asp Arg Leu Pro Pro Leu Pro Val Thr Pro Gly Met

100

105

110

119/546

Glu Gly Ala Gly Val Val Ile Ala Val Gly Glu Gly Val Ser Asp Arg
115 120 125

Lys Ala Gly Asp Arg Val Met Val Leu Asn Arg Ser Gly Met Trp Gln
130 135 140

Glu Glu Val Thr Val Pro Ser Val Gln Thr Phe Leu Ile Pro Glu Ala
145 150 155 160

Met Thr Phe Glu Glu Ala Ala Ala Leu Leu Val Asn Tyr Ile Thr Ala
165 170 175

Tyr Met Val Leu Phe Asp Phe Gly Asn Leu Gln Pro Gly His Ser Val
180 185 190

Leu Val His Met Ala Ala Gly Gly Val Gly Met Ala Ala Val Gln Leu
195 200 205

Cys Arg Thr Val Glu Asn Val Thr Val Phe Gly Thr Ala Ser Ala Ser
210 215 220

Lys His Glu Ala Leu Lys Glu Asn Gly Val Thr His Pro Ile Asp Tyr
225 230 235 240

His Thr Thr Asp Tyr Val Asp Glu Ile Lys Lys Ile Ser Pro Lys Gly
245 250 255

Val Asp Ile Val Met Asp Pro Leu Gly Gly Ser Asp Thr Ala Lys Gly

260

265

270

Tyr Asn Leu Leu Lys Pro Met Gly Lys Val Val Thr Tyr Gly Met Ala

275

280

285

Asn Leu Leu Thr Gly Pro Lys Arg Asn Leu Met Ala Leu Ala Arg Thr

290

295

300

Trp Trp Asn Gln Phe Ser Val Thr Ala Leu Gln Leu Leu Gln Ala Asn

305

310

315

320

Arg Ala Val Cys Gly Phe His Leu Gly Tyr Leu Asp Gly Glu Val Glu

325

330

335

Leu Val Ser Gly Val Val Ala Arg Leu Leu Ala Leu Tyr Asn Gln Gly

340

345

350

His Ile Lys Pro His Ile Asp Ser Val Trp Pro Phe Glu Lys Val Ala

355

360

365

Asp Ala Met Lys Gln Met Gln Glu Lys Lys Asn Val Gly Lys Val Leu

370

375

380

Leu Val Pro Gly Pro Glu Lys Glu Asn

385

390

<210> 44

<211> 2396

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (50).. (1228)

<400> 44

agctgtgcac tctccatcca gctgtgcgct ctcgtcggga gtcccagcc atg tcc gac 58
Met Ser Asp

1

gag aga gag gta gcc gag gca gcg acc ggg gaa gac gcc tct tcg ccg 106
Glu Arg Glu Val Ala Glu Ala Ala Thr Gly Glu Asp Ala Ser Ser Pro

5

10

15

cct ccg aaa acc gag gca gcg agc gac ccc cag cat ccc gcg gcc tcc 154
Pro Pro Lys Thr Glu Ala Ala Ser Asp Pro Gln His Pro Ala Ala Ser

20

25

30

35

gaa ggg gcc gcc gcc gcc gcc gcc tcg ccg cca ctg ctg cgc tgc cta 202
Glu Gly Ala Ala Ala Ala Ala Ser Pro Pro Leu Leu Arg Cys Leu

40

45

50

gtg ctc acc ggc ttt gga ggc tac gac aag gtg aag ctg cag agc cgg 250
Val Leu Thr Gly Phe Gly Gly Tyr Asp Lys Val Lys Leu Gln Ser Arg

55

60

65

ccg gca gcg ccc ccg gcc cct ggg ccc ggc cag ctg acg ctg cgt ctg 298

Pro Ala Ala Pro Pro Ala Pro Gly Pro Gly Gln Leu Thr Leu Arg Leu
 70 75 80

cgg gcc tgc ggg ctc aac ttc gca gac ctc atg gct agg cag ggg ctg 346
 Arg Ala Cys Gly Leu Asn Phe Ala Asp Leu Met Ala Arg Gln Gly Leu
 85 90 95

tac gac cgt ctc ccg cct ctg cct gtc act ccg ggc atg gag ggc gcg 394
 Tyr Asp Arg Leu Pro Pro Leu Pro Val Thr Pro Gly Met Glu Gly Ala
 100 105 110 115

ggt gtt gtg atc gca gtg ggc gag gga gtc agc gac cgc aag gca gga 442
 Gly Val Val Ile Ala Val Gly Glu Gly Val Ser Asp Arg Lys Ala Gly
 120 125 130

gac cgg gtg atg gtg ttg aac ccg tca ggg atg tgg cag gaa gag gtg 490
 Asp Arg Val Met Val Leu Asn Arg Ser Gly Met Trp Gln Glu Glu Val
 135 140 145

act gtg ccc tgc gtc cag acc ttc ctg att cct gag gcc atg acc ttt 538
 Thr Val Pro Ser Val Gln Thr Phe Leu Ile Pro Glu Ala Met Thr Phe
 150 155 160

gag gaa gct gct gcc ttg ctc gtc aat tac att aca gcc tac atg gtc 586
 Glu Glu Ala Ala Ala Leu Leu Val Asn Tyr Ile Thr Ala Tyr Met Val
 165 170 175

ctc ttt gac ttc ggc aac cta cag cct ggc cac agc gtc ttg gta cac 634
 Leu Phe Asp Phe Gly Asn Leu Gln Pro Gly His Ser Val Leu Val His

180 185 190 195

atg gct gca ggg ggt gtg ggt atg gct gcc gtg cag ctg tgc cgt aca 682
Met Ala Ala Gly Gly Val Gly Met Ala Ala Val Gln Leu Cys Arg Thr

200 205 210

gtg gag aat gtg aca gtg ttc gga acg gcc tcg gcc agc aag cac gag 730
Val Glu Asn Val Thr Val Phe Gly Thr Ala Ser Ala Ser Lys His Glu

215 220 225

gca ctg aag gag aat ggg gtc aca cat ccc atc gac tat cac acg act 778
Ala Leu Lys Glu Asn Gly Val Thr His Pro Ile Asp Tyr His Thr Thr

230 235 240

gac tac gtg gat gag atc aag aag att tcc cct aaa gga gtg gac att 826
Asp Tyr Val Asp Glu Ile Lys Lys Ile Ser Pro Lys Gly Val Asp Ile

245 250 255

gtc atg gac cct ctg ggt ggg tca gat act gcc aag ggc tac aac ctc 874
Val Met Asp Pro Leu Gly Gly Ser Asp Thr Ala Lys Gly Tyr Asn Leu

260 265 270 275

ctg aaa ccc atg ggc aaa gtc gtc acc tat gga atg gcc aac ctg ctg 922
Leu Lys Pro Met Gly Lys Val Val Thr Tyr Gly Met Ala Asn Leu Leu

280 285 290

acg ggc ccc aaa cgg aac ctg atg gcc ctg gcc cgg aca tgg tgg aat 970
Thr Gly Pro Lys Arg Asn Leu Met Ala Leu Ala Arg Thr Trp Trp Asn

295 300 305

cag ttc agc gtg aca gct ctg cag ctg ctg cag gcc aac cgg gct gtg 1018

Gln Phe Ser Val Thr Ala Leu Gln Leu Leu Gln Ala Asn Arg Ala Val

310

315

320

tgt ggc ttc cac ctg ggc tac ctg gat ggt gag gtg gag ctg gtc agt 1066

Cys Gly Phe His Leu Gly Tyr Leu Asp Gly Glu Val Glu Leu Val Ser

325

330

335

ggt gtg gtg gcc cgc ctc ctg gct ctg tac aac cag ggc cac atc aag 1114

Gly Val Val Ala Arg Leu Leu Ala Leu Tyr Asn Gln Gly His Ile Lys

340

345

350

355

ccc cac att gac tca gtc tgg ccc ttc gag aag gtg gct gat gcc atg 1162

Pro His Ile Asp Ser Val Trp Pro Phe Glu Lys Val Ala Asp Ala Met

360

365

370

aaa cag atg cag gag aag aag aat gtg ggc aag gtc ctc ctg gtt cca 1210

Lys Gln Met Gln Glu Lys Lys Asn Val Gly Lys Val Leu Leu Val Pro

375

380

385

ggg cca gag aag gag aac tagggcaagt ggctgtgaga ccctagagac 1258

Gly Pro Glu Lys Glu Asn

390

cagcgaaggg agaagttggg aagctacgtt ctgttggcca ccagacttgc atttcagcct 1318

ctgtcataat gctctgccct ccctcccccg aagttctctg tggatgac cgtctcccc 1378

tgccccctccc cgccttccga cctctgaaga ggttgggaag tgaccatttg gatgtctggg 1438

ccctgccaaag gcgacaggga gggtcagagg gaggccggct gcttccctgcc cccacctttt 1498

ccccggggcct gcctgtctgc ttttgtcca aggttagcca gtccccctg ttgtgttcca 1558

ttgtctttca cctctgcctc atctttcctc ccgtccctgc cccgccacct ccccaaagaa 1618

ttgaaacgtc agctcaggat atggggccaa tctctgtgag tccagcatgt acctgtctct 1678

ccctagtgtc ccttcagcct gggctgacca gtgcccgct ctgggcttga ccagttccca 1738

atctcgctct ctgtcccaa cttcttaagc acaattgggc ttcttccatc tccaggtttt 1798

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ccctcatgtg gtcctgtcca tgtcccgct ctatgggtgt tgaggagaaa ggcggggaag 1918

cttctcagc cttgcagata tgtgtggcat ttactagcca gagctctgaa aggcagtgtc 1978

gtctgtttct tgtactggga ccaaagtaaa aatccaagca cattccccctt gcagttaggg 2038

gaggccctac tgccttctca aagcagagag gcagcttctc aaactcagcc caaaactctg 2098

tttcatggg tggggagatg gagcaggga gtacagagtg ggttggtcag gacctgggccc 2158

attgcaacca aaatggggac ttcttgggta gggaggctac tccctctact cactgagcta 2218

ggattaggga gggttattgc cccaaccatt gcaatgggag gtggaggagc aggcctcagcc 2278

tcctcattgt ctaaagagg cctaaatgtg tgaagigcga ttcttgcttt tgtgtacccc 2338

accaccccat taccacagct gccitttgtgt gtttgtgtca ataaaaagcc aaaccctg 2396

<210> 45

<211> 393

<212> PRT

<213> Homo sapiens

<400> 45

Met Ser Asp Glu Arg Glu Val Ala Glu Ala Ala Thr Gly Glu Asp Ala

1

5

10

15

Ser Ser Pro Pro Pro Lys Thr Glu Ala Ala Ser Asp Pro Gln His Pro

20

25

30

Ala Ala Ser Glu Gly Ala Ala Ala Ala Ala Ala Ser Pro Pro Leu Leu

35

40

45

Arg Cys Leu Val Leu Thr Gly Phe Gly Gly Tyr Asp Lys Val Lys Leu

50

55

60

Gln Ser Arg Pro Ala Ala Pro Pro Ala Pro Gly Pro Gly Gln Leu Thr

65

70

75

80

Leu Arg Leu Arg Ala Cys Gly Leu Asn Phe Ala Asp Leu Met Ala Arg

85

90

95

Gln Gly Leu Tyr Asp Arg Leu Pro Pro Leu Pro Val Thr Pro Gly Met
100 105 110

Glu Gly Ala Gly Val Val Ile Ala Val Gly Glu Gly Val Ser Asp Arg
115 120 125

Lys Ala Gly Asp Arg Val Met Val Leu Asn Arg Ser Gly Met Trp Gln
130 135 140

Glu Glu Val Thr Val Pro Ser Val Gln Thr Phe Leu Ile Pro Glu Ala
145 150 155 160

Met Thr Phe Glu Glu Ala Ala Ala Leu Leu Val Asn Tyr Ile Thr Ala
165 170 175

Tyr Met Val Leu Phe Asp Phe Gly Asn Leu Gln Pro Gly His Ser Val
180 185 190

Leu Val His Met Ala Ala Gly Gly Val Gly Met Ala Ala Val Gln Leu
195 200 205

Cys Arg Thr Val Glu Asn Val Thr Val Phe Gly Thr Ala Ser Ala Ser
210 215 220

Lys His Glu Ala Leu Lys Glu Asn Gly Val Thr His Pro Ile Asp Tyr
225 230 235 240

His Thr Thr Asp Tyr Val Asp Glu Ile Lys Lys Ile Ser Pro Lys Gly

245 250 255
Val Asp Ile Val Met Asp Pro Leu Gly Gly Ser Asp Thr Ala Lys Gly
260 265 270
Tyr Asn Leu Leu Lys Pro Met Gly Lys Val Val Thr Tyr Gly Met Ala
275 280 285
Asn Leu Leu Thr Gly Pro Lys Arg Asn Leu Met Ala Leu Ala Arg Thr
290 295 300
Trp Trp Asn Gln Phe Ser Val Thr Ala Leu Gln Leu Leu Gln Ala Asn
305 310 315 320
Arg Ala Val Cys Gly Phe His Leu Gly Tyr Leu Asp Gly Glu Val Glu
325 330 335
Leu Val Ser Gly Val Val Ala Arg Leu Leu Ala Leu Tyr Asn Gln Gly
340 345 350
His Ile Lys Pro His Ile Asp Ser Val Trp Pro Phe Glu Lys Val Ala
355 360 365
Asp Ala Met Lys Gln Met Gln Glu Lys Lys Asn Val Gly Lys Val Leu
370 375 380
Leu Val Pro Gly Pro Glu Lys Gln Asn
385 390

<210> 46

<211> 2396

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (50).. (1228)

<400> 46

agctgtgcac tctccatcca gctgtgcgct ctcgtcggga gtcccagcc atg tcc gac 58

Met Ser Asp

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gag aga gag gta gcc gag gca gcg acc ggg gaa gac gcc tct tcg ccg 106

Glu Arg Glu Val Ala Glu Ala Ala Thr Gly Glu Asp Ala Ser Ser Pro

5

10

15

cct ccg aaa acc gag gca gcg agc gac ccc cag cat ccc gcg gcc tcc 154

Pro Pro Lys Thr Glu Ala Ala Ser Asp Pro Gln His Pro Ala Ala Ser

20

25

30

35

gaa ggg gcc gcc gcc gcc gcc gcc tcg ccg cca ctg ctg cgc tgc cta 202

Glu Gly Ala Ala Ala Ala Ala Ser Pro Pro Leu Leu Arg Cys Leu

40

45

50

gtg ctc acc gcc ttt gga ggc tac gac aag gtg aag ctg cag agc cgg 250

Val Leu Thr Gly Phe Gly Gly Tyr Asp Lys Val Lys Leu Gln Ser Arg

55

60

65

ccg gca gcg ccc ccg gcc cct ggg ccc ggc cag ctg acg ctg cgt ctg 298
 Pro Ala Ala Pro Pro Ala Pro Gly Pro Gly Gln Leu Thr Leu Arg Leu
 70 75 80

cgg gcc tgc ggg ctc aac ttc gca gac ctc atg gct agg cag ggg ctg 346
 Arg Ala Cys Gly Leu Asn Phe Ala Asp Leu Met Ala Arg Gln Gly Leu
 85 90 95

tac gac cgt ctc ccg cct ctg cct gtc act ccg ggc atg gag ggc gcc 394
 Tyr Asp Arg Leu Pro Pro Leu Pro Val Thr Pro Gly Met Glu Gly Ala
 100 105 110 115

ggt gtt gtg atc gca gtg ggc gag gga gtc agc gac cgc aag gca gga 442
 Gly Val Val Ile Ala Val Gly Glu Gly Val Ser Asp Arg Lys Ala Gly
 120 125 130

gac cgg gtg atg gtg ttg aac cgg tca ggg atg tgg cag gaa gag gtg 490
 Asp Arg Val Met Val Leu Asn Arg Ser Gly Met Trp Gln Glu Glu Val
 135 140 145

act gtg ccc tcg gtc cag acc ttc ctg att cct gag gcc atg acc ttt 538
 Thr Val Pro Ser Val Gln Thr Phe Leu Ile Pro Glu Ala Met Thr Phe
 150 155 160

gag gaa gct gct gcc ttg ctc gtc aat tac att aca gcc tac atg gtc 586
 Glu Glu Ala Ala Ala Leu Leu Val Asn Tyr Ile Thr Ala Tyr Met Val
 165 170 175

ctc ttt gac ttc ggc aac cta cag cct ggc cac agc gtc ttg gla cac 634
 Leu Phe Asp Phe Gly Asn Leu Gln Pro Gly His Ser Val Leu Val His
 180 185 190 195

atg gct gca ggg ggt gtg ggt atg gct gcc gtg cag ctg tgc cgt aca 682
 Met Ala Ala Gly Gly Val Gly Met Ala Ala Val Gln Leu Cys Arg Thr
 200 205 210

gtg gag aat gtg aca gtg ttc gga acg gcc tcg gcc agc aag cac gag 730
 Val Glu Asn Val Thr Val Phe Gly Thr Ala Ser Ala Ser Lys His Glu
 215 220 225

gca ctg aag gag aat ggg gtc aca cat ccc atc gac tat cac acg act 778
 Ala Leu Lys Glu Asn Gly Val Thr His Pro Ile Asp Tyr His Thr Thr
 230 235 240

gac tac gtg gat gag atc aag aag att tcc cct aaa gga gtg gac att 826
 Asp Tyr Val Asp Glu Ile Lys Lys Ile Ser Pro Lys Gly Val Asp Ile
 245 250 255

gtc atg gac cct ctg ggt ggg tca gat act gcc aag ggc tac aac ctc 874
 Val Met Asp Pro Leu Gly Gly Ser Asp Thr Ala Lys Gly Tyr Asn Leu
 260 265 270 275

ctg aaa ccc atg ggc aaa gtc gtc acc tat gga atg gcc aac ctg ctg 922
 Leu Lys Pro Met Gly Lys Val Val Thr Tyr Gly Met Ala Asn Leu Leu
 280 285 290

acg ggc ccc aaa cgg aac ctg atg gcc ctg gcc cgg aca tgg tgg aat 970
Thr Gly Pro Lys Arg Asn Leu Met Ala Leu Ala Arg Thr Trp Trp Asn
295 300 305

cag ttc agc gtg aca gct ctg cag ctg ctg cag gcc aac cgg gct gtg 1018
Gln Phe Ser Val Thr Ala Leu Gln Leu Leu Gln Ala Asn Arg Ala Val
310 315 320

tgt ggc ttc cac ctg ggc tac ctg gat ggt gag gtg gag ctg gtc agt 1066
Cys Gly Phe His Leu Gly Tyr Leu Asp Gly Glu Val Glu Leu Val Ser
325 330 335

ggt gtg gtg gcc cgc ctc ctg gct ctg tac aac cag ggc cac atc aag 1114
Gly Val Val Ala Arg Leu Leu Ala Leu Tyr Asn Gln Gly His Ile Lys
340 345 350 355

ccc cac att gac tca gtc tgg ccc ttc gag aag gtg gct gat gcc atg 1162
Pro His Ile Asp Ser Val Trp Pro Phe Glu Lys Val Ala Asp Ala Met
360 365 370

aaa cag atg cag gag aag aag aat gtg ggc aag gtc ctc ctg gtt cca 1210
Lys Gln Met Gln Glu Lys Lys Asn Val Gly Lys Val Leu Leu Val Pro
375 380 385

ggg cca gag aag cag aac tagggcaagt ggctgtgaga ccctagagac 1258
Gly Pro Glu Lys Gln Asn
390

cagcgaaggg agaagttggg aagctacgtt ctgttgcca ccagacttgc atttcagcct 1318

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cttctcagc ctgcagata tgtgtggcat ttactagcca gagctctgaa aggcagtgt 1978

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ggattagga gggttattgc cccaaccatt gcaatgggag gtggaggac aggtcagcc 2278

tcctcattgt ctaaagagg cctaaatgtg tgaagtcga ttcttgcttt tgtgtacccc 2338

accaccccat taccacagct gcccttgtgt gtttgtgtca ataaaaagcc aaaccctg 2396

<210> 47

<211> 138

<212> PRT

<213> Homo sapiens

<400> 47

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Phe	Gly	Val	Phe	Phe	Leu	Phe	Phe	Gly	Met	Ile	Leu	Phe	Phe	Asp	Lys
				20					25					30	

Ala	Leu	Leu	Ala	Ile	Gly	Asn	Val	Leu	Phe	Val	Ala	Gly	Leu	Ala	Phe
				35				40					45		

Val	Ile	Gly	Leu	Glu	Arg	Thr	Phe	Arg	Phe	Phe	Phe	Gln	Lys	His	Lys
				50				55				60			

Met	Lys	Ala	Thr	Gly	Phe	Phe	Leu	Gly	Gly	Val	Phe	Val	Val	Leu	Ile
				65			70			75				80	

Gly Trp Pro Leu Ile Gly Met Ile Phe Glu Ile Tyr Gly Phe Phe Leu
85 90 95

Leu Phe Arg Gly Phe Phe Pro Val Val Val Gly Phe Ile Arg Arg Val
100 105 110

Pro Val Leu Gly Ser Leu Leu Asn Leu Pro Gly Ile Arg Ser Phe Val
115 120 125

Asp Lys Val Gly Glu Ser Asn Asn Met Val
130 135

<210> 48

<211> 2976

<212> DNA

<213> Homo sapiens

<220>

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<222> (110).. (523)

<400> 48

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Met Ile Ser

1

tta acg gac acg cag aaa att gga atg gga tta aca gga ttt gga gtg 166
Leu Thr Asp Thr Gln Lys Ile Gly Met Gly Leu Thr Gly Phe Gly Val

5

10

15

ttt ttc ctg ttc ttt gga atg att ctc ttt ttt gac aaa gca cta ctg 214
Phe Phe Leu Phe Phe Gly Met Ile Leu Phe Phe Asp Lys Ala Leu Leu

20

25

30

35

gct att gga aat gtt tta ttt gta gcc ggc ttg gct ttt gta att ggt 262
Ala Ile Gly Asn Val Leu Phe Val Ala Gly Leu Ala Phe Val Ile Gly

40

45

50

tta gaa aga aca ttc aga ttc ttc ttc caa aaa cat aaa atg aaa gct 310
Leu Glu Arg Thr Phe Arg Phe Phe Phe Gln Lys His Lys Met Lys Ala

55

60

65

aca ggt ttt ttt ctg ggt ggt gta ttt gta gtc ctt att ggt tgg cct 358
Thr Gly Phe Phe Leu Gly Gly Val Phe Val Val Leu Ile Gly Trp Pro

70

75

80

ttg ata ggc atg atc ttc gaa att tat gga ttt ttt ctc ttg ttc agg 406
Leu Ile Gly Met Ile Phe Glu Ile Tyr Gly Phe Phe Leu Leu Phe Arg

85

90

95

ggc ttc ttt cct gtc gtt gtt ggc ttt att aga aga gtg cca gtc ctt 454
Gly Phe Phe Pro Val Val Val Gly Phe Ile Arg Arg Val Pro Val Leu

100

105

110

115

gga tcc ctc cta aat tta cct gga att aga tca ttt gta gat aaa gtt 502
Gly Ser Leu Leu Asn Leu Pro Gly Ile Arg Ser Phe Val Asp Lys Val
120 125 130

gga gaa agc aac aat atg gta taacaacaag tgaatttgaa gactcattta 553
Gly Glu Ser Asn Asn Met Val
135

aaatattgtg ttatttataa agtcatttga agaatttca gcacaaaatt aaattacatg 613

aaatagcttg taatgttctt tacaggagtt taaaacgtat agcctacaaa gtaccagcag 673

caaattagca aagaagcagt gaaaacaggc ttctactcaa gtgaactaag aagaagtcag 733

caagcaaact gagagaggtg aaatccatgt taatgatgct taagaaactc ttgaaggcta 793

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gtccactgca atggcaaaaa tatttccagt tgcactgtat ctcctggaagt gatgcatgaa 973

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atatttcaaa gccaggtgaa aatctgaact agatattctt tgttggaata tgcaaaggtc 1153

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aaagtctcat acttcttggg agtctgccct cctaagtatc tgtctatata attcattacg 1273

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tgiccatgat taatttttct ttcttcttcc ttttttttaa attttagcag tggcttatta 1453

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taaaaggta aacttatggc tgtttttaaa gggctattca tttaatciga gttttccctt 1573

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taaactgact atggittctt aagaacatga cactaaaaaa aaagtggitt ttttcaccg 1753

tigctgatta ttagacagta ggaaatagct gttttcttta gttttacaag atgtgacagc 1813

tttagtgga gatgtaggga aacatttcaa cagccatagt actatttgtt ttaccactga 1873

tigcactgtt ttgttttttt aacagttgca aagcttttta atgcataaaa gtataattga 1933

aatctgtggt atttatttac aaacatgtct acaaaaatag attacagctt attttatitt 1993

tagttaaatc tottaataca cagagaactc ccaacttgc tcacttaaat aaggaaagac 2053

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gaatgttttt ctttccct tataaattgt aattcctgaa atactgctgc tttaaaaagt 2893
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2976

<210> 49

<211> 359

<212> PRT

<213> Homo sapiens

<400> 49

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His Ala Phe Leu Lys Ile Asn Gln Ala Lys Pro Glu Cys Gly Arg Gln
20 25 30

Ser Leu Val Glu Leu Leu Ile Arg Pro Val Gln Arg Leu Pro Ser Val
35 40 45

Ala Leu Leu Leu Asn Asp Leu Lys Lys His Thr Ala Asp Glu Asn Pro
50 55 60

Asp Lys Ser Thr Leu Glu Lys Ala Ile Gly Ser Leu Lys Glu Val Met
65 70 75 80

Thr His Ile Asn Glu Asp Lys Arg Lys Thr Glu Ala Gln Lys Gln Ile
85 90 95

Phe Asp Val Val Tyr Glu Val Asp Gly Cys Pro Ala Asn Leu Leu Ser

100 105 110
Ser His Arg Ser Leu Val Gln Arg Val Glu Thr Ile Ser Leu Gly Glu
115 120 125
His Pro Cys Asp Arg Gly Glu Gln Val Thr Leu Phe Leu Phe Asn Asp
130 135 140
Cys Leu Glu Ile Ala Arg Lys Arg His Lys Val Ile Gly Thr Phe Arg
145 150 155 160
Ser Pro His Gly Gln Thr Arg Pro Pro Ala Ser Leu Lys His Ile His
165 170 175
Leu Met Pro Leu Ser Gln Ile Lys Lys Val Leu Asp Ile Arg Glu Thr
180 185 190
Glu Asp Cys His Asn Ala Phe Ala Leu Leu Val Arg Pro Pro Thr Glu
195 200 205
Gln Ala Asn Val Leu Leu Ser Phe Gln Met Thr Ser Asp Glu Leu Pro
210 215 220
Lys Glu Asn Trp Leu Lys Met Leu Cys Arg His Val Ala Asn Thr Ile
225 230 235 240
Cys Lys Ala Asp Ala Glu Asn Leu Ile Tyr Thr Ala Asp Pro Glu Ser
245 250 255

Phe Glu Val Asn Thr Lys Asp Met Asp Ser Thr Leu Ser Arg Ala Ser
260 265 270

Arg Ala Ile Lys Lys Thr Ser Lys Lys Val Thr Arg Ala Phe Ser Phe
275 280 285

Ser Lys Thr Pro Lys Arg Ala Leu Arg Arg Ala Leu Met Thr Ser His
290 295 300

Gly Ser Val Glu Gly Arg Ser Pro Ser Ser Asn Asp Lys His Val Met
305 310 315 320

Ser Arg Leu Ser Ser Thr Ser Ser Leu Ala Gly Ile Pro Ser Pro Ser
325 330 335

Leu Val Ser Leu Pro Ser Phe Phe Glu Arg Arg Ser His Thr Leu Ser
340 345 350

Arg Ser Thr Thr His Leu Ile
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<210> 50

<211> 2636

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> (327).. (1403)

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atgttaatat attggcaaca attattcagt tatttcaagt accattggaa gaggaaggac 120

aacgtggtagg acctatcctt gcaccagagg agattaagac tatttttggg agcatcccag 180

atacttttga tgtacacact aagataaagg atgatcttga agaccttata gttaattggg 240

atgagagcaa aagcattggg gacatttttc tgaaatattc aaaagatttg gtaaaaacct 300

accctccctt tgtaaacttc ttgaa atg agc aag gaa aca att att aaa tgt 353

Met Ser Lys Glu Thr Ile Ile Lys Cys

1

5

gaa aaa cag aaa cca aga ttt cat gct ttt ctc aag ata aac caa gca 401

Glu Lys Gln Lys Pro Arg Phe His Ala Phe Leu Lys Ile Asn Gln Ala

10

15

20

25

aaa cca gaa tgt gga cgg cag agc ctt gtt gaa ctt ctt atc cga cca 449

Lys Pro Glu Cys Gly Arg Gln Ser Leu Val Glu Leu Leu Ile Arg Pro

30

35

40

gta cag agg tta ccc agt gtt gca tta ctt tta aat gat ctt aag aag 497

Val Gln Arg Leu Pro Ser Val Ala Leu Leu Leu Asn Asp Leu Lys Lys

45

50

55

cat aca gct gat gaa aat cca gac aaa agc act tta gaa aaa gct att 545
 His Thr Ala Asp Glu Asn Pro Asp Lys Ser Thr Leu Glu Lys Ala Ile

60

65

70

gga tca ctg aag gaa gta atg acg cat att aat gag gat aag aga aaa 593
 Gly Ser Leu Lys Glu Val Met Thr His Ile Asn Glu Asp Lys Arg Lys

75

80

85

aca gaa gct caa aag caa att ttt gat gtt gtt tat gaa gta gat gga 641
 Thr Glu Ala Gln Lys Gln Ile Phe Asp Val Val Tyr Glu Val Asp Gly

90

95

100

105

tgc cca gct aat ctt tta tct tct cac cga agc tta gta cag cgg gtt 689
 Cys Pro Ala Asn Leu Leu Ser Ser His Arg Ser Leu Val Gln Arg Val

110

115

120

gaa aca att tct cta ggt gag cac ccc tgt gac aga gga gaa caa gta 737
 Glu Thr Ile Ser Leu Gly Glu His Pro Cys Asp Arg Gly Glu Gln Val

125

130

135

act ctc ttc ctc ttc aat gat tgc cta gag ata gca aga aaa cgg cac 785
 Thr Leu Phe Leu Phe Asn Asp Cys Leu Glu Ile Ala Arg Lys Arg His

140

145

150

aag gtt att ggc act ttt agg agt cct cat ggc caa acc cga ccc cca 833
 Lys Val Ile Gly Thr Phe Arg Ser Pro His Gly Gln Thr Arg Pro Pro

155

160

165

gct tct ctt aag cat att cac cta atg cct ctt tct cag att aag aag 881

Ala Ser Leu Lys His Ile His Leu Met Pro Leu Ser Gln Ile Lys Lys
 170 175 180 185

gta ttg gac ata aga gag aca gaa gat tgc cat aat gct ttt gcc ttg 929
 Val Leu Asp Ile Arg Glu Thr Glu Asp Cys His Asn Ala Phe Ala Leu
 190 195 200

ctt gtg agg cca cca aca gag cag gca aat gtg cta ctc agt ttc cag 977
 Leu Val Arg Pro Pro Thr Glu Gln Ala Asn Val Leu Leu Ser Phe Gln
 205 210 215

atg aca tca gat gaa ctt cca aaa gaa aac tgg cta aag atg ctg tgt 1025
 Met Thr Ser Asp Glu Leu Pro Lys Glu Asn Trp Leu Lys Met Leu Cys
 220 225 230

cga cat gta gct aac acc att tgt aaa gca gat gct gag aat ctt att 1073
 Arg His Val Ala Asn Thr Ile Cys Lys Ala Asp Ala Glu Asn Leu Ile
 235 240 245

tat act gct gat cca gaa tcc ttt gaa gta aat aca aaa gat atg gac 1121
 Tyr Thr Ala Asp Pro Glu Ser Phe Glu Val Asn Thr Lys Asp Met Asp
 250 255 260 265

agt aca ttg agt aga gca tca aga gca ata aaa aag act tca aaa aag 1169
 Ser Thr Leu Ser Arg Ala Ser Arg Ala Ile Lys Lys Thr Ser Lys Lys
 270 275 280

gtt aca aga gca ttc tct ttc tcc aaa act cca aaa aga gct ctt cga 1217
 Val Thr Arg Ala Phe Ser Phe Ser Lys Thr Pro Lys Arg Ala Leu Arg

285

290

295

agg gct ctt atg aca tcc cac ggc tca gtg gag gga aga agt cct tcc 1265
Arg Ala Leu Met Thr Ser His Gly Ser Val Glu Gly Arg Ser Pro Ser
300 305 310

agc aat gat aag cat gta atg agt cgt ctt tct agc aca tca tca tta 1313
Ser Asn Asp Lys His Val Met Ser Arg Leu Ser Ser Thr Ser Ser Leu
315 320 325

gca ggt atc cct tct ccc tcc ctt gtc agc ctt cct tcc ttc ttt gaa 1361
Ala Gly Ile Pro Ser Pro Ser Leu Val Ser Leu Pro Ser Phe Phe Glu
330 335 340 345

agg aga agt cat acg tta agt aga tct aca act cat ttg ata 1403
Arg Arg Ser His Thr Leu Ser Arg Ser Thr Thr His Leu Ile
350 355

tgaagcgtaa ccaaaatctt aaattataga aatgtataga cacctcatatc tcaaataaga 1463

aactgactta aatggtactt gtaattagca cttggtgaaa gctggaagga agataaataa 1523

cactaaacta tgctatttga tttttcttct tgaaagagta aggtttacct gttacatttt 1583

caagttaatt catgtaaaaa atgatagta ttttgatgta atttatctct tgtttgaatc 1643

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gtatccatga atgaatttat ggaaatagat atttgtgcag ctcaatttat gcagagattt 1823

aatgacatca taatactgga tgaaaacttg catagaattc tgattaaata gtgggtctgt 1883

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catttaaagg agattgtttc aaaatatatt tgcaaattga gataaggaca gaaagattga 2063

gaaacattgt atattttgca aaaacaagat gttttagct gtttcagaga gactacggta 2123

tatttatggt aattttatcc actagcaaatt cttgatttag ttgatagtg tgtggaattt 2183

tattttgaag gataagacca tgggaaaatt gtggtaaaga ctgittgtac ccttcatgaa 2243

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caaagtgtga tatctttcac aatagccttt ttatagtcag taattcagaa taatcaagtt 2423

catatggata aatgcatttt tatttccat ttttttaggg agtgcataaa atgtttgtca 2483

cttaaatttc aagtttctgt tttaatagtt aactgactat agattgtttt ctatgccatg 2543

tatgtgccac ttctgagagt agtaaatgac tctttgtac attttaaaag caattgtatt 2603

agtaagaact ttgtaaataa atacctaaaa ccc

2636

<210> 51

<211> 883

<212> PRT

<213> Homo sapiens

<400> 51

Met Ala Glu Asn Ser Val Leu Thr Ser Thr Thr Gly Arg Thr Ser Leu

1

5

10

15

Ala Asp Ser Ser Ile Phe Asp Ser Lys Val Thr Glu Ile Ser Lys Glu

20

25

30

Asn Leu Leu Ile Gly Ser Thr Ser Tyr Val Glu Glu Glu Met Pro Gln

35

40

45

Ile Glu Thr Arg Val Ile Leu Val Gln Glu Ala Gly Lys Gln Glu Glu

50

55

60

Leu Thr Lys Ala Leu Lys Asp Ile Lys Val Gly Phe Val Lys Met Glu

65

70

75

80

Ser Val Glu Glu Phe Glu Gly Leu Asp Ser Pro Glu Phe Glu Asn Val

85

90

95

Phe Val Val Thr Asp Phe Gln Asp Ser Val Phe Asn Asp Leu Tyr Lys

100

105

110

Ala Asp Cys Arg Val Ile Gly Pro Pro Val Val Leu Asn Cys Ser Gln
115 120 125

Lys Gly Glu Pro Leu Pro Phe Ser Cys Arg Pro Leu Tyr Cys Thr Ser
130 135 140

Met Met Asn Leu Val Leu Cys Phe Thr Gly Phe Arg Lys Lys Glu Glu
145 150 155 160

Leu Val Arg Leu Val Thr Leu Val His His Met Gly Gly Val Ile Arg
165 170 175

Lys Asp Phe Asn Ser Lys Val Thr His Leu Val Ala Asn Cys Thr Gln
180 185 190

Gly Glu Lys Phe Arg Val Ala Val Ser Leu Gly Thr Pro Ile Met Lys
195 200 205

Pro Glu Trp Ile Tyr Lys Ala Trp Glu Arg Arg Asn Glu Gln Asp Phe
210 215 220

Tyr Ala Ala Val Asp Asp Phe Arg Asn Glu Phe Lys Val Pro Pro Phe
225 230 235 240

Gln Asp Cys Ile Phe Ser Phe Leu Gly Phe Ser Asp Glu Glu Lys Thr
245 250 255

Asn Met Glu Glu Met Thr Glu Met Gln Gly Gly Lys Tyr Leu Pro Leu

260

265

270

Gly Asp Glu Arg Cys Thr His Leu Val Val Glu Glu Asn Ile Val Lys

275

280

285

Asp Leu Pro Phe Glu Pro Ser Lys Lys Leu Tyr Val Val Lys Gln Glu

290

295

300

Trp Phe Trp Gly Ser Ile Gln Met Asp Ala Arg Ala Gly Glu Thr Met

305

310

315

320

Tyr Leu Tyr Glu Lys Ala Asn Thr Pro Glu Leu Lys Lys Ser Val Ser

325

330

335

Met Leu Ser Leu Asn Thr Pro Asn Ser Asn Arg Lys Arg Arg Arg Leu

340

345

350

Lys Glu Thr Leu Ala Gln Leu Ser Arg Asp Thr Asp Val Ser Pro Phe

355

360

365

Pro Pro Arg Lys Arg Pro Ser Ala Glu His Ser Leu Ser Ile Gly Ser

370

375

380

Leu Leu Asp Ile Ser Asn Thr Pro Glu Ser Ser Ile Asn Tyr Gly Asp

385

390

395

400

Thr Pro Lys Ser Cys Thr Lys Ser Ser Lys Ser Ser Thr Pro Val Pro

405

410

415

Ser Lys Gln Ser Ala Arg Trp Gln Val Ala Lys Glu Leu Tyr Gln Thr
420 425 430

Glu Ser Asn Tyr Val Asn Ile Leu Ala Thr Ile Ile Gln Leu Phe Gln
435 440 445

Val Pro Leu Glu Glu Glu Gly Gln Arg Gly Gly Pro Ile Leu Ala Pro
450 455 460

Glu Glu Ile Lys Thr Ile Phe Gly Ser Ile Pro Asp Ile Phe Asp Val
465 470 475 480

His Thr Lys Ile Lys Asp Asp Leu Glu Asp Leu Ile Val Asn Trp Asp
485 490 495

Glu Ser Lys Ser Ile Gly Asp Ile Phe Leu Lys Tyr Ser Lys Asp Leu
500 505 510

Val Lys Thr Tyr Pro Pro Phe Val Asn Phe Phe Glu Met Ser Lys Glu
515 520 525

Thr Ile Ile Lys Cys Glu Lys Gln Lys Pro Arg Phe His Ala Phe Leu
530 535 540

Lys Ile Asn Gln Ala Lys Pro Glu Cys Gly Arg Gln Ser Leu Val Glu
545 550 555 560

Leu Leu Ile Arg Pro Val Gln Arg Leu Pro Ser Val Ala Leu Leu Leu
565 570 575

Asn Asp Leu Lys Lys His Thr Ala Asp Glu Asn Pro Asp Lys Ser Thr
580 585 590

Leu Glu Lys Ala Ile Gly Ser Leu Lys Glu Val Met Thr His Ile Asn
595 600 605

Glu Asp Lys Arg Lys Thr Glu Ala Gln Lys Gln Ile Phe Asp Val Val
610 615 620

Tyr Glu Val Asp Gly Cys Pro Ala Asn Leu Leu Ser Ser His Arg Ser
625 630 635 640

Leu Val Gln Arg Val Glu Thr Ile Ser Leu Gly Glu His Pro Cys Asp
645 650 655

Arg Gly Glu Gln Val Thr Leu Phe Leu Phe Asn Asp Cys Leu Glu Ile
660 665 670

Ala Arg Lys Arg His Lys Val Ile Gly Thr Phe Arg Ser Pro His Gly
675 680 685

Gln Thr Arg Pro Pro Ala Ser Leu Lys His Ile His Leu Met Pro Leu
690 695 700

Ser Gln Ile Lys Lys Val Leu Asp Ile Arg Glu Thr Glu Asp Cys His
705 710 715 720

Asn Ala Phe Ala Leu Leu Val Arg Pro Pro Thr Glu Gln Ala Asn Val

725

730

735

Leu Leu Ser Phe Gln Met Thr Ser Asp Glu Leu Pro Lys Glu Asn Trp

740

745

750

Leu Lys Met Leu Cys Arg His Val Ala Asn Thr Ile Cys Lys Ala Asp

755

760

765

Ala Glu Asn Leu Ile Tyr Thr Ala Asp Pro Glu Ser Phe Glu Val Asn

770

775

780

Thr Lys Asp Met Asp Ser Thr Leu Ser Arg Ala Ser Arg Ala Ile Lys

785

790

795

800

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810

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820

825

830

Gly Arg Ser Pro Ser Ser Asn Asp Lys His Val Met Ser Arg Leu Ser

835

840

845

Ser Thr Ser Ser Leu Ala Gly Ile Pro Ser Pro Ser Leu Val Ser Leu

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tat gta gaa gaa gag atg cct cag att gaa aca aga gtg ata ttg gtt 196

Tyr Val Glu Glu Glu Met Pro Gln Ile Glu Thr Arg Val Ile Leu Val

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caa gaa gct gga aaa caa gaa gaa ctt aca aaa gcc tta aag gac att 244
Gln Glu Ala Gly Lys Gln Glu Glu Leu Thr Lys Ala Leu Lys Asp Ile

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Ser Val Phe Asn Asp Leu Tyr Lys Ala Asp Cys Arg Val Ile Gly Pro

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cca gtt gta tta aat tgt tca caa aaa gga gag cct ttg cca ttt tca 436
Pro Val Val Leu Asn Cys Ser Gln Lys Gly Glu Pro Leu Pro Phe Ser

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Cys Arg Pro Leu Tyr Cys Thr Ser Met Met Asn Leu Val Leu Cys Phe

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act gga ttt agg aaa aaa gaa gaa cta gtc agg ttg gtg aca ttg gtc 532
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 His His Met Gly Gly Val Ile Arg Lys Asp Phe Asn Ser Lys Val Thr
 170 175 180

cat ttg gtg gca aat tgt aca caa gga gaa aaa ttc agg gtt gct gtg 628
 His Leu Val Ala Asn Cys Thr Gln Gly Glu Lys Phe Arg Val Ala Val
 185 190 195 200

agt cta ggt act cca att atg aag cca gaa tgg att tat aaa gct tgg 676
 Ser Leu Gly Thr Pro Ile Met Lys Pro Glu Trp Ile Tyr Lys Ala Trp
 205 210 215

gaa agg cgg aat gaa cag gat ttc tat gca gca gtt gat gac ttt aga 724
 Glu Arg Arg Asn Glu Gln Asp Phe Tyr Ala Ala Val Asp Asp Phe Arg
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aat gaa ttt aaa gtt cct cca ttt caa gat tgt att ttt agt ttc ctg 772
 Asn Glu Phe Lys Val Pro Pro Phe Gln Asp Cys Ile Phe Ser Phe Leu
 235 240 245

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 Gly Phe Ser Asp Glu Glu Lys Thr Asn Met Glu Glu Met Thr Glu Met
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 Gln Gly Gly Lys Tyr Leu Pro Leu Gly Asp Glu Arg Cys Thr His Leu
 265 270 275 280

gta gtt gaa gag aat ata gta aaa gat ctt ccc ttt gaa cct tca aag 916

Val Val Glu Glu Asn Ile Val Lys Asp Leu Pro Phe Glu Pro Ser Lys
285 290 295

aaa ctt tat gtt gtc aag caa gag tgg ttc tgg gga agc att caa atg 964
Lys Leu Tyr Val Val Lys Gln Glu Trp Phe Trp Gly Ser Ile Gln Met
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Asp Ala Arg Ala Gly Glu Thr Met Tyr Leu Tyr Glu Lys Ala Asn Thr
315 320 325

cct gag ctc aag aaa tca gtg tca atg ctt tct cta aat acc cct aac 1060
Pro Glu Leu Lys Lys Ser Val Ser Met Leu Ser Leu Asn Thr Pro Asn
330 335 340

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Ser Asn Arg Lys Arg Arg Arg Leu Lys Glu Thr Leu Ala Gln Leu Ser
345 350 355 360

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365 370 375

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Glu His Ser Leu Ser Ile Gly Ser Leu Leu Asp Ile Ser Asn Thr Pro
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Ala Thr Ile Ile Gln Leu Phe Gln Val Pro Leu Glu Glu Glu Gly Gln
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Ser Ile Pro Asp Ile Phe Asp Val His Thr Lys Ile Lys Asp Asp Leu
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Phe Leu Lys Tyr Ser Lys Asp Leu Val Lys Thr Tyr Pro Pro Phe Val
505 510 515 520

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aaa cca aga ttt cat gct ttt ctc aag ata aac caa gca aaa cca gaa 1684
Lys Pro Arg Phe His Ala Phe Leu Lys Ile Asn Gln Ala Lys Pro Glu
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Cys Gly Arg Gln Ser Leu Val Glu Leu Leu Ile Arg Pro Val Gln Arg
555 560 565

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570 575 580

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Lys Glu Val Met Thr His Ile Asn Glu Asp Lys Arg Lys Thr Glu Ala
605 610 615

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635 640 645

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Ser Leu Gly Glu His Pro Cys Asp Arg Gly Glu Gln Val Thr Leu Phe
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ctc ttc aat gat tgc cta gag ata gca aga aaa cgg cac aag gtt att 2068
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685 690 695

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700 705 710

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Ile Arg Glu Thr Glu Asp Cys His Asn Ala Phe Ala Leu Leu Val Arg
715 720 725

cca cca aca gag cag gca aat gtg cta ctc agt ttc cag atg aca tca 2260
Pro Pro Thr Glu Gln Ala Asn Val Leu Leu Ser Phe Gln Met Thr Ser
730 735 740

gat gaa ctt cca aaa gaa aac tgg cta aag atg ctg tgt cga cat gta 2308

Asp Glu Leu Pro Lys Glu Asn Trp Leu Lys Met Leu Cys Arg His Val
 745 750 755 760

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gat cca gaa tcc ttt gaa gta aat aca aaa gat atg gac agt aca ttg 2404
 Asp Pro Glu Ser Phe Glu Val Asn Thr Lys Asp Met Asp Ser Thr Leu
 780 785 790

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 Ala Phe Ser Phe Ser Lys Thr Pro Lys Arg Ala Leu Arg Arg Ala Leu
 810 815 820

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 Met Thr Ser His Gly Ser Val Glu Gly Arg Ser Pro Ser Ser Asn Asp
 825 830 835 840

aag cat gta atg agt cgt ctt tct agc aca tca tca tta gca ggt atc 2596
 Lys His Val Met Ser Arg Leu Ser Ser Thr Ser Ser Leu Ala Gly Ile
 845 850 855

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865

870

cat acg tta agt aga tct aca act cat ttg ata tgaagcgta ccaaaatctt 2697
His Thr Leu Ser Arg Ser Thr Thr His Leu Ile

875

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Ser Asn Cys Asp Ile Val Lys Ala Thr Gln Tyr Gly Ile Phe Glu Arg
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Cys Lys Glu Leu Val Glu Ala Gly Tyr Asp Val Arg Gln Pro Asp Lys
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Glu Asn Val Ser Leu Leu His Trp Ala Ala Ile Asn Asn Arg Leu Asp
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Gly Asp Leu Asn Ser Thr Pro Leu His Trp Ala Ile Arg Gln Gly His
115 120 125

Leu Pro Met Val Ile Leu Leu Leu Gln His Gly Ala Asp Pro Thr Leu
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Ile Asp Gly Glu Gly Phe Ser Ser Ile His Leu Ala Val Leu Phe Gln
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His Met Pro Ile Ile Ala Tyr Leu Ile Ser Lys Gly Gln Ser Val Asn
165 170 175

Met Thr Asp Val Asn Gly Gln Thr Pro Leu Met Leu Ser Ala His Lys
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Val Ile Gly Pro Glu Pro Thr Gly Phe Leu Leu Lys Phe Asn Pro Ser
195 200 205

Leu Asn Val Val Asp Lys Ile His Gln Asn Thr Pro Leu His Trp Ala
210 215 220

Val Ala Ala Gly Asn Val Asn Ala Val Asp Lys Leu Leu Glu Ala Gly
225 230 235 240

Ser Ser Leu Asp Ile Gln Asn Val Lys Gly Glu Thr Pro Leu Asp Met
245 250 255

Ala Leu Gln Asn Lys Asn Gln Leu Ile Ile His Met Leu Lys Thr Glu
260 265 270

Ala Lys Met Arg Ala Asn Gln Lys Phe Arg Leu Trp Arg Trp Leu Gln
275 280 285

Lys Cys Glu Leu Phe Leu Leu Leu Met Leu Ser Val Ile Thr Met Trp
290 295 300

Ala Ile Gly Tyr Ile Leu Asp Phe Asn Ser Asp Ser Trp Leu Leu Lys
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Gly Cys Leu Leu Val Thr Leu Phe Phe Leu Thr Ser Leu Phe Pro Arg

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330

335

Phe Leu Val Gly Tyr Lys Asn Leu Val Tyr Leu Pro Thr Ala Phe Leu

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345

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Leu Ser Ser Val Phe Trp Ile Phe Met Thr Trp Phe Ile Leu Phe Phe

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360

365

Pro Asp Leu Ala Gly Ala Pro Phe Tyr Phe Ser Phe Ile Phe Ser Ile

370

375

380

Val Ala Phe Leu Tyr Phe Phe Tyr Lys Thr Trp Ala Thr Asp Pro Gly

385

390

395

400

Phe Thr Lys Ala Ser Glu Glu Glu Lys Lys Val Asn Ile Ile Thr Leu

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Ala Glu Thr Gly Ser Leu Asp Phe Arg Thr Phe Cys Thr Ser Cys Leu

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Phe Gly Asn His His Tyr Tyr Ile Phe Phe Leu Phe Phe Leu Ser Met

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475

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Val Cys Gly Trp Ile Ile Tyr Gly Ser Phe Ile Tyr Leu Ser Ser His
485 490 495

Cys Ala Thr Thr Phe Lys Glu Asp Gly Leu Trp Thr Tyr Leu Asn Gln
500 505 510

Ile Val Ala Cys Ser Pro Trp Val Leu Tyr Ile Leu Met Leu Ala Thr
515 520 525

Phe His Phe Ser Trp Ser Thr Phe Leu Leu Leu Asn Gln Leu Phe Gln
530 535 540

Ile Ala Phe Leu Gly Leu Thr Ser His Glu Arg Ile Ser Leu Gln Lys
545 550 555 560

Gln Ser Lys His Met Lys Gln Thr Leu Ser Leu Arg Lys Thr Pro Tyr
565 570 575

Asn Leu Gly Phe Met Gln Asn Leu Ala Asp Phe Phe Gln Cys Gly Cys
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Met Glu Gly Pro

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ggg ctg ggc tgc cag tgc agg aat cac agc cat ggc ccc cac cct cca 163
Gly Leu Gly Ser Gln Cys Arg Asn His Ser His Gly Pro His Pro Pro

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aat gca aga gaa gct ctt cct ctt ata gag gac tct agt aac tgt gac 259
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Val Glu Ala Gly Tyr Asp Val Arg Gln Pro Asp Lys Glu Asn Val Ser

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Leu Leu His Trp Ala Ala Ile Asn Asn Arg Leu Asp Leu Val Lys Phe

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115

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Ser Thr Pro Leu His Trp Ala Ile Arg Gln Gly His Leu Pro Met Val

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ata tta tta ctc cag cat ggt gca gac ccc act ctt att gat gga gag 547

Ile Leu Leu Leu Gln His Gly Ala Asp Pro Thr Leu Ile Asp Gly Glu

135

140

145

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Gly Phe Ser Ser Ile His Leu Ala Val Leu Phe Gln His Met Pro Ile

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165

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190

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gat aaa ata cac caa aac act cca ctt cac tgg gca gtt gca gca gga 787
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220

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230

235

240

atc cag aat gtt aag gga gaa aca cct ctt gat atg gct cta caa aac 883
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250

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260

aaa aat cag ctc att att cat atg cta aaa aca gaa gcc aaa atg aga 931
 Lys Asn Gln Leu Ile Ile His Met Leu Lys Thr Glu Ala Lys Met Arg

265

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275

gcc aac caa aag ttc aga ctt tgg agg tgg ctg cag aaa tgc gag ctc 979
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280

285

290

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295 300 305

ata ttg gac ttc aat tca gat tct tgg ctt tta aaa gga tgt ctt cta 1075
Ile Leu Asp Phe Asn Ser Asp Ser Trp Leu Leu Lys Gly Cys Leu Leu
310 315 320

gta aca ctg ttt ttt ctg aca tct ttg ttt cca agg ttc ttg gtt ggg 1123
Val Thr Leu Phe Phe Leu Thr Ser Leu Phe Pro Arg Phe Leu Val Gly
325 330 335 340

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Tyr Lys Asn Leu Val Tyr Leu Pro Thr Ala Phe Leu Leu Ser Ser Val
345 350 355

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Phe Trp Ile Phe Met Thr Trp Phe Ile Leu Phe Phe Pro Asp Leu Ala
360 365 370

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Gly Ala Pro Phe Tyr Phe Ser Phe Ile Phe Ser Ile Val Ala Phe Leu
375 380 385

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Tyr Phe Phe Tyr Lys Thr Trp Ala Thr Asp Pro Gly Phe Thr Lys Ala
390 395 400

tct gaa gaa gaa aag aaa gtg aat atc atc acc ctt gca gaa act ggc 1363

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 405 410 415 420

tct ctg gac ttc aga aca ttt tgt aca tca tgt ctt ata agg aag cca 1411
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 425 430 435

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 440 445 450

gat caa cac tgc ctg tgg act gga cgg tgc ata ggt ttt ggc aac cat 1507
 Asp Gln His Cys Leu Trp Thr Gly Arg Cys Ile Gly Phe Gly Asn His
 455 460 465

cac tat tac ata ttc ttc ttg ttt ttc ctt tcc atg gta tgt ggc tgg 1555
 His Tyr Tyr Ile Phe Phe Leu Phe Phe Leu Ser Met Val Cys Gly Trp
 470 475 480

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 Ile Ile Tyr Gly Ser Phe Ile Tyr Leu Ser Ser His Cys Ala Thr Thr
 485 490 495 500

ttc aaa gaa gat gga tta tgg act tac ctc aat cag att gtg gcc tgt 1651
 Phe Lys Glu Asp Gly Leu Trp Thr Tyr Leu Asn Gln Ile Val Ala Cys
 505 510 515

tcc cct tgg gtt tta tat atc ttg atg cta gca act ttc cat ttc tca 1699
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520

525

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tgg tca aca ttt tta tta tta aat caa ctc ttt cag att gcc ttt ctg 1747

Trp Ser Thr Phe Leu Leu Leu Asn Gln Leu Phe Gln Ile Ala Phe Leu

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540

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ggc ctg acc tcc cat gag aga atc agc ctg cag aag cag agc aag cat 1795

Gly Leu Thr Ser His Glu Arg Ile Ser Leu Gln Lys Gln Ser Lys His

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555

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atg aaa cag acg ttg tcc ctc agg aag aca cca tac aat ctt gga ttc 1843

Met Lys Gln Thr Leu Ser Leu Arg Lys Thr Pro Tyr Asn Leu Gly Phe

565

570

575

580

atg cag aac ctg gca gat ttc ttt cag tgt ggc tgc ttt ggc ttg gtg 1891

Met Gln Asn Leu Ala Asp Phe Phe Gln Cys Gly Cys Phe Gly Leu Val

585

590

595

aag ccc tgt gtg gta gat tgg aca tca cag tac acc atg gtc ttt cac 1939

Lys Pro Cys Val Val Asp Trp Thr Ser Gln Tyr Thr Met Val Phe His

600

605

610

cca gcc agg gag aag gtt ctt cgc tca gta tgaagaaaag caacccaaaa 1989

Pro Ala Arg Glu Lys Val Leu Arg Ser Val

615

620

ctctcaatct gatttgtttt tgtttatgtc gatgccctgt agtttgaaag tgaagtaaag 2049

atttagaatt cacctaagtc caaaggaaaa cacgtggttt ttaaagccat taggtaaaaa 2109

aagttctcaa taaaggcatt acaatttttt aggttttagaa agatggactt ttctgataaa 2169
 tcttggcaga catctaaaaa aaaaaccata tttttcacia gaaaatgcaa gttacttttt 2229
 ttggaaataa tactcactga ttatggataa aatggaatat tttcagatac tatattggct 2289
 gtttcaaaat agtactattc tttaaacttg taatttttgc taagttattt gtctttgttg 2349
 tatctataaa tatgtaaaaa atattttaa ataggttacct gttttgcttt cacacttaat 2409
 aaaaaatttt tttttgt 2426

<210> 55

<211> 257

<212> PRT

<213> Homo sapiens

<400> 55

Met Ala Ser Lys Ile Gly Ser Arg Arg Trp Met Leu Gln Leu Ile Met

1 5 10 15

Gln Leu Gly Ser Val Leu Leu Thr Arg Cys Pro Phe Trp Gly Cys Phe

20 25 30

Ser Gln Leu Met Leu Tyr Ala Glu Arg Ala Glu Ala Arg Arg Lys Pro

35 40 45

Asp Ile Pro Val Pro Tyr Leu Tyr Phe Asp Met Gly Ala Ala Val Leu

50

55

60

Cys Ala Ser Phe Met Ser Phe Gly Val Lys Arg Arg Trp Phe Ala Leu

65

70

75

80

Gly Ala Ala Leu Gln Leu Ala Ile Ser Thr Tyr Ala Ala Tyr Ile Gly

85

90

95

Gly Tyr Val His Tyr Gly Asp Trp Leu Lys Val Arg Met Tyr Ser Arg

100

105

110

Thr Val Ala Ile Ile Gly Gly Phe Leu Val Leu Ala Ser Gly Ala Gly

115

120

125

Glu Leu Tyr Arg Arg Lys Pro Arg Ser Arg Ser Leu Gln Ser Thr Gly

130

135

140

Gln Val Phe Leu Gly Ile Tyr Leu Ile Cys Val Ala Tyr Ser Leu Gln

145

150

155

160

His Ser Lys Glu Asp Arg Leu Ala Tyr Leu Asn His Leu Pro Gly Gly

165

170

175

Glu Leu Met Ile Gln Leu Phe Phe Val Leu Tyr Gly Ile Leu Ala Leu

180

185

190

Ala Phe Leu Ser Gly Tyr Tyr Val Thr Leu Ala Ala Gln Ile Leu Ala

195

200

205

Val Leu Leu Pro Pro Val Met Leu Leu Ile Asp Gly Asn Val Ala Tyr
 210 215 220

Trp His Asn Thr Arg Arg Val Glu Phe Trp Asn Gln Met Lys Leu Leu
 225 230 235 240

Gly Glu Ser Val Gly Ile Phe Gly Thr Ala Val Ile Leu Ala Thr Asp
 245 250 255

Gly

<210> 56

<211> 1520

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (10).. (780)

<400> 56

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Met Ala Ser Lys Ile Gly Ser Arg Arg Trp Met Leu Gln Leu

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10

atc atg cag ttg ggt tcg glg ctg ctc aca cgc tgc ccc ttt tgg ggc 99

Ile Met Gln Leu Gly Ser Val Leu Leu Thr Arg Cys Pro Phe Trp Gly
 15 20 25 30

tgc ttc agc cag ctc atg ctg tac gct gag agg gct gag gca cgc cgg 147
 Cys Phe Ser Gln Leu Met Leu Tyr Ala Glu Arg Ala Glu Ala Arg Arg
 35 40 45

aag ccc gac atc cca gtg cct tac ctg tat ttc gac atg ggg gca gcc 195
 Lys Pro Asp Ile Pro Val Pro Tyr Leu Tyr Phe Asp Met Gly Ala Ala
 50 55 60

gtg ctg tgc gct agt ttc atg tcc ttt ggc gtg aag cgg cgc tgg ttc 243
 Val Leu Cys Ala Ser Phe Met Ser Phe Gly Val Lys Arg Arg Trp Phe
 65 70 75

gcg ctg ggg gcc gca ctc caa ttg gcc att agc acc tac gcc gcc tac 291
 Ala Leu Gly Ala Ala Leu Gln Leu Ala Ile Ser Thr Tyr Ala Ala Tyr
 80 85 90

atc ggg ggc tac gtc cac tac ggg gac tgg ctg aag gtc cgt atg tac 339
 Ile Gly Gly Tyr Val His Tyr Gly Asp Trp Leu Lys Val Arg Met Tyr
 95 100 105 110

tgc cgc aca gtt gcc atc atc ggc ggc ttt ctt gtg ttg gcc agc ggt 387
 Ser Arg Thr Val Ala Ile Ile Gly Gly Phe Leu Val Leu Ala Ser Gly
 115 120 125

gct ggg gag ctg tac cgc cgg aaa cct cgc agc cgc tcc ctg cag tcc 435
 Ala Gly Glu Leu Tyr Arg Arg Lys Pro Arg Ser Arg Ser Leu Gln Ser

130

135

140

acc ggc cag gtg ttc ctg ggt atc tac ctc atc tgt gtg gcc tac tca 483
Thr Gly Gln Val Phe Leu Gly Ile Tyr Leu Ile Cys Val Ala Tyr Ser

145

150

155

ctg cag cac agc aag gag gac cgg ctg gcg tat ctg aac cat ctc cca 531
Leu Gln His Ser Lys Glu Asp Arg Leu Ala Tyr Leu Asn His Leu Pro

160

165

170

gga ggg gag ctg atg atc cag ctg ttc ttc gtg ctg tat ggc atc ctg 579
Gly Gly Glu Leu Met Ile Gln Leu Phe Phe Val Leu Tyr Gly Ile Leu

175

180

185

190

gcc ctg gcc ttt ctg tca ggc tac tac gtg acc ctc gct gcc cag atc 627
Ala Leu Ala Phe Leu Ser Gly Tyr Tyr Val Thr Leu Ala Ala Gln Ile

195

200

205

ctg gct gta ctg ctg ccc cct gtc atg ctg ctc att gat ggc aat gtt 675
Leu Ala Val Leu Leu Pro Pro Val Met Leu Leu Ile Asp Gly Asn Val

210

215

220

gct tac tgg cac aac acg cgg cgt gtt gag ttc tgg aac cag atg aag 723
Ala Tyr Trp His Asn Thr Arg Arg Val Glu Phe Trp Asn Gln Met Lys

225

230

235

ctc ctt gga gag agt gtg ggc atc ttc gga act gct gtc atc ctg gcc 771
Leu Leu Gly Glu Ser Val Gly Ile Phe Gly Thr Ala Val Ile Leu Ala

240

245

250

act gat ggc tgagttttat ggcaagaggc tgagatgggc acagggagcc 820

Thr Asp Gly

255

actgagggtc accctgcctt cctccttgct ggcccagctg ctgtttattt atgctttttg 880

gtctgtttgt ttgatctttt gcttttttaa aattgttttt tgcagttaag aggcagctca 940

tttgtccaaa tttctgggct cagcgcctgg gagggcagga gccctggcac taatgctgta 1000

caggtttttt tctgttagg agagctgagg ccagctgccc actgagtctc ctgtccctga 1060

gaagggagta tggcagggct gggatgcggc tactgagagt gggagagtgg gagacagagg 1120

aaggaagatg gagattggaa gtgagcaaat gtgaaaaatt cctctttgaa cctggcagat 1180

gcagctaggc tctgcagtgc tgtttggaga ctgtgagagg gagtgtgtgt gttgacacat 1240

gtggatcagg cccaggaagg gcacaggggc tgagcactac agaagtcaca tgggttctca 1300

gggtatgcca ggggcagaaa cagtaccggc tctctgtcac tcacctgag agtagagcag 1360

accctgttct gctctgggct gtgaaggggt ggagcaggca gtggccagct ttgcccttcc 1420

tgctgtctct gtictagct ccatggttgg cctgggtggg gtggagtcc ctcccaaaca 1480

ccagaccaca cagtcctcca aaaataaaca ttttatatag 1520

<210> 57

<211> 107

<212> PRT

<213> Homo sapiens

<400> 57

Met Ala Leu Phe Ala Gly Gly Lys Leu Arg Val His Leu Asp Ile Gln
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Val Gly Glu His Ala Asn Asn Tyr Pro Glu Ile Ala Ala Lys Asp Lys
 20 25 30

Leu Thr Glu Leu Gln Leu Arg Ala Arg Gln Leu Leu Asp Gln Val Glu
 35 40 45

Gln Ile Gln Lys Glu Gln Asp Tyr Gln Arg Tyr Arg Glu Glu Arg Phe
 50 55 60

Arg Leu Thr Ser Glu Ser Thr Asn Gln Arg Val Leu Trp Trp Ser Ile
 65 70 75 80

Ala Gln Thr Val Ile Leu Ile Leu Thr Gly Ile Trp Gln Met Arg His
 85 90 95

Leu Lys Ser Phe Phe Glu Ala Lys Lys Leu Val
 100 105

<210> 58
 <211> 1496
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (9).. (329)

<400> 58

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 Met Ala Leu Phe Ala Gly Gly Lys Leu Arg Val His Leu Asp
 1 5 10

atc cag gtt ggg gag cat gcc aac aac tac cct gag att gct gca aaa 98
 Ile Gln Val Gly Glu His Ala Asn Asn Tyr Pro Glu Ile Ala Ala Lys
 15 20 25 30

gat aag ctg acg gag cta cag ctc cgc gcc cgc cag ttg ctt gat cag 146
 Asp Lys Leu Thr Glu Leu Gln Leu Arg Ala Arg Gln Leu Leu Asp Gln
 35 40 45

gtg gaa cag att cag aag gag cag gat tac caa agg tat cgt gaa gag 194
 Val Glu Gln Ile Gln Lys Glu Gln Asp Tyr Gln Arg Tyr Arg Glu Glu
 50 55 60

cgc ttc cga ctg acg agc gag agc acc aac cag agg gtc cta tgg tgg 242
 Arg Phe Arg Leu Thr Ser Glu Ser Thr Asn Gln Arg Val Leu Trp Trp
 65 70 75

tcc att gct cag act gtc atc ctc atc ctc act ggc atc tgg cag atg 290
 Ser Ile Ala Gln Thr Val Ile Leu Ile Leu Thr Gly Ile Trp Gln Met

80

85

90

cgt cac ctc aag agc ttc ttt gag gcc aag aag ctg gtg tagtgccctc 339
 Arg His Leu Lys Ser Phe Phe Glu Ala Lys Lys Leu Val

95

100

105

tttgatgac ccttcctttt tacctcattt atttggtaact tccccacac agtcctttat 399

ccacctggat ttttagggaa aaaaaatgaa aaagaataag tcacattggt tccatggcca 459

caaaccattc agatcagcca ctgtctgacc ctggttctta aggacacatg acattagtcc 519

aatctttcaa aatcttgtct tagggcttgt gaggaatcag aactaacca ggactcagtc 579

ctgcttcttt tgcctcgagt gattttcttc tgtttttcac taaataagca aatgaaaact 639

ctctccatta ccttctgctt tctctttgtc cacttacgca gtaggtgact ggcatgtgcc 699

acagagcagg ccttgcctca ctgtctgctg gtcagttctg ggttactta atggctttgt 759

gaatgtaaat aaggggcagg tcttggccct agaggattga gatgttttc tatactttag 819

aactattttt ggataaatta tataatttcc ttccatgtag aagtgttact gacctgaact 879

agctcaaaat accaatgcag ttcttgcatt ctgggttttg ttttctttt tttttttt 939

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 ataaaacatg ttgtaat 1496

<210> 59

<211> 272

<212> PRT

<213> Homo sapiens

<400> 59

Met Met Ile His Gly Phe Gln Ser Ser His Arg Asp Phe Cys Phe Gly

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5

10

15

Pro Trp Lys Leu Thr Ala Ser Lys Thr His Ile Met Lys Ser Ala Asp
20 25 30

Val Glu Lys Leu Ala Asp Glu Leu His Met Pro Ser Leu Pro Glu Met
35 40 45

Met Phe Gly Asp Asn Val Leu Arg Ile Gln His Gly Ser Gly Phe Gly
50 55 60

Ile Glu Phe Asn Ala Thr Asp Ala Leu Arg Cys Val Asn Asn Tyr Gln
65 70 75 80

Gly Met Leu Lys Val Ala Cys Ala Glu Glu Trp Gln Glu Ser Arg Thr
85 90 95

Glu Gly Glu His Ser Lys Glu Val Ile Lys Pro Tyr Asp Trp Thr Tyr
100 105 110

Thr Thr Asp Tyr Lys Gly Thr Leu Leu Gly Glu Ser Leu Lys Leu Lys
115 120 125

Val Val Pro Thr Thr Asp His Ile Asp Thr Glu Lys Leu Lys Ala Arg
130 135 140

Glu Gln Ile Lys Phe Phe Glu Glu Val Leu Leu Phe Glu Asp Glu Leu
145 150 155 160

His Asp His Gly Val Ser Ser Leu Ser Val Lys Ile Arg Val Met Pro

165

170

175

Ser Ser Phe Phe Leu Leu Leu Arg Phe Phe Leu Arg Ile Asp Gly Val

180

185

190

Leu Ile Arg Met Asn Asp Thr Arg Leu Tyr His Glu Ala Asp Lys Thr

195

200

205

Tyr Met Leu Arg Glu Tyr Thr Ser Arg Glu Ser Lys Ile Ser Ser Leu

210

215

220

Met His Val Pro Pro Ser Leu Phe Thr Glu Pro Asn Glu Ile Ser Gln

225

230

235

240

Tyr Leu Pro Ile Lys Glu Ala Val Cys Glu Lys Leu Ile Phe Pro Glu

245

250

255

Arg Ile Asp Pro Asn Pro Ala Asp Ser Gln Lys Ser Thr Gln Val Glu

260

265

270

<210> 60

<211> 1916

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (117).. (932)

<400> 60

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gccgccgccg ctgttcagc ttattccttg tggcctctgc gggtcctgcc tcagcc atg 119

Met

1

atg atc cac ggc ttc cag agc agc cac cgg gat ttc tgc ttc ggg ccc 167

Met Ile His Gly Phe Gln Ser Ser His Arg Asp Phe Cys Phe Gly Pro

5

10

15

tgg aag ctg acg gcg tcc aag acc cac atc atg aag tcg gcg gat gtg 215

Trp Lys Leu Thr Ala Ser Lys Thr His Ile Met Lys Ser Ala Asp Val

20

25

30

gag aaa tta gcc gat gaa tta cat atg cca tct ctc cct gaa atg atg 263

Glu Lys Leu Ala Asp Glu Leu His Met Pro Ser Leu Pro Glu Met Met

35

40

45

ttt gga gac aac gtt tta aga atc cag cat ggg tct ggc ttt gga att 311

Phe Gly Asp Asn Val Leu Arg Ile Gln His Gly Ser Gly Phe Gly Ile

50

55

60

65

gag ttc aat gct aca gat gcg tta aga tgt gta aac aac tac caa gga 359

Glu Phe Asn Ala Thr Asp Ala Leu Arg Cys Val Asn Asn Tyr Gln Gly

70

75

80

atg ctt aaa gtg gcc tgt gct gaa gag tgg caa gaa agc agg acg gag 407

Met Leu Lys Val Ala Cys Ala Glu Glu Trp Gln Glu Ser Arg Thr Glu

85

90

95

ggt gaa cac tcc aaa gag gtt att aaa cca tat gat tgg acc tat aca 455

Gly Glu His Ser Lys Glu Val Ile Lys Pro Tyr Asp Trp Thr Tyr Thr

100

105

110

aca gat tat aag gga acc tta ctt gga gaa tct ctt aag tta aag gtt 503

Thr Asp Tyr Lys Gly Thr Leu Leu Gly Glu Ser Leu Lys Leu Lys Val

115

120

125

gta cct aca aca gat cat ata gat aca gaa aaa ttg aaa gcc aga gaa 551

Val Pro Thr Thr Asp His Ile Asp Thr Glu Lys Leu Lys Ala Arg Glu

130

135

140

145

cag att aag ttt ttt gaa gaa gtt ctc ctt ttt gag gat gaa ctt cat 599

Gln Ile Lys Phe Phe Glu Glu Val Leu Leu Phe Glu Asp Glu Leu His

150

155

160

gat cat gga gtt tca agc ctg agt gtg aag att aga gla atg cct tct 647

Asp His Gly Val Ser Ser Leu Ser Val Lys Ile Arg Val Met Pro Ser

165

170

175

agc ttt ttc ctg ctg ttg cgg ttt ttc ttg aga att gat ggg gtg ctt 695

Ser Phe Phe Leu Leu Leu Arg Phe Phe Leu Arg Ile Asp Gly Val Leu

180

185

190

atc aga atg aat gac acg aga ctt tac cat gag gct gac aag acc tac 743

Ile Arg Met Asn Asp Thr Arg Leu Tyr His Glu Ala Asp Lys Thr Tyr

195	200	205	
atg tta cga gaa tat acg tca cga gaa agc aaa att tct agt ttg atg 791			
Met Leu Arg Glu Tyr Thr Ser Arg Glu Ser Lys Ile Ser Ser Leu Met			
210	215	220	225
cat gtt cca cct tcc ctc ttc acg gaa cct aat gaa ata tcc cag tat 839			
His Val Pro Pro Ser Leu Phe Thr Glu Pro Asn Glu Ile Ser Gln Tyr			
230	235	240	
tta cca ata aag gaa gca gtt tgt gag aag cta ata ttt cca gaa aga 887			
Leu Pro Ile Lys Glu Ala Val Cys Glu Lys Leu Ile Phe Pro Glu Arg			
245	250	255	
att gat cct aac cca gca gac tca caa aaa agt aca caa gtg gaa 932			
Ile Asp Pro Asn Pro Ala Asp Ser Gln Lys Ser Thr Gln Val Glu			
260	265	270	
taaaatgtga tacaacatat actcactatg gaatctgact ggacaccttg gctatttgta 992			
aggggttatt tttattatga gaattaattg ccttgtttat gtacagattt tctgtagcct 1052			
taaaggaaaa aaaaataaag atcgttacag gcaggtttca ctcaactgct atttgtactg 1112			
tctgtcttca cattcatatt ccagatttat attttctgga gttaaatttg gatgatttct 1172			
aaattatcac aaagtgggac ctcagcagta gtgatgtgtg tgtctcatga gcagtgagca 1232			
cagtctgcat tcatcatgaa acactatctt ctaccaggag gaggttaatg taaatcacca 1292			

aatcccaatg ccttgtgact ttcataggat tcttgalcat gcatgttgat gtactggctc 1352
ttcactttgg gctttctgat gtttattcac accttggag agttgcaact tgccacatac 1412
gaaattagtc tcatagtga gigaactica accccaaat tttaaaaatg tatttcccc 1472
cagttttaa ttgccttga aatttaaaaa aaaaaatta gacttagtac cagaacaaa 1532
aatacctaga ttttggaga acctattaca tacatagaaa catgaatatg gtttaccwct 1592
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tcttggcccc tgaatagtc tagattactt atttgagaa ttgattgtta aaaattacag 1712
ggaattaaaa taattgccct tttttttta gagggtaaga gatgggtaga agagtatgcc 1772
tctgaaaatt ttattagttt attcttgttg agaatacaca gaaaatgtgt atttgcctat 1832
tgctaaatat gatatatgcc attttgtatt tatttgcctc aagtgtcttt tttaagagg 1892
agaataaaca ataaggaatt actg 1916

<210> 61

<211> 219

<212> PRT

<213> Homo sapiens

<400> 61

Met Asn Arg Leu Phe Gly Lys Ala Lys Pro Lys Ala Pro Pro Pro Ser

1

5

10

15

Leu Thr Asp Cys Ile Gly Thr Val Asp Ser Arg Ala Glu Ser Ile Asp

20

25

30

Lys Lys Ile Ser Arg Leu Asp Ala Glu Leu Val Lys Tyr Lys Asp Gln

35

40

45

Ile Lys Lys Met Arg Glu Gly Pro Ala Lys Asn Met Val Lys Gln Lys

50

55

60

Ala Leu Arg Val Leu Lys Gln Lys Arg Met Tyr Glu Gln Gln Arg Asp

65

70

75

80

Asn Leu Ala Gln Gln Ser Phe Asn Met Glu Gln Ala Asn Tyr Thr Ile

85

90

95

Gln Ser Leu Lys Asp Thr Lys Thr Thr Val Asp Ala Met Lys Leu Gly

100

105

110

Val Lys Glu Met Lys Lys Ala Tyr Lys Gln Val Lys Ile Asp Gln Ile

115

120

125

Glu Asp Leu Gln Asp Gln Leu Glu Asp Met Met Glu Asp Ala Asn Glu

130

135

140

Ile Gln Glu Ala Leu Ser Arg Ser Tyr Gly Thr Pro Glu Leu Asp Glu

145

150

155

160

Asp Asp Leu Glu Ala Glu Leu Asp Ala Leu Gly Asp Glu Leu Leu Ala

165

170

175

Asp Glu Asp Ser Ser Tyr Leu Asp Glu Ala Ala Ser Ala Pro Ala Ile

180

185

190

Pro Glu Gly Val Pro Thr Asp Thr Lys Asn Lys Asp Gly Val Leu Val

195

200

205

Asp Glu Phe Gly Leu Pro Gln Ile Pro Ala Ser

210

215

<210> 62

<211> 1362

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (49).. (705)

<400> 62

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Met Asn Arg

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ctc ttc ggg aaa gcg aaa ccc aag gct ccg ccg ccc agc ctg act gac 105
 Leu Phe Gly Lys Ala Lys Pro Lys Ala Pro Pro Pro Ser Leu Thr Asp

5

10

15

tgc att ggc acg gtg gac agt aga gca gaa tcc att gac aag aag att 153
 Cys Ile Gly Thr Val Asp Ser Arg Ala Glu Ser Ile Asp Lys Lys Ile

20

25

30

35

tct cga ttg gat gct gag cta gtg aag tat aag gat cag atc aag aag 201
 Ser Arg Leu Asp Ala Glu Leu Val Lys Tyr Lys Asp Gln Ile Lys Lys

40

45

50

atg aga gag ggt cct gca aag aat atg gtc aag cag aaa gcc ttg cga 249
 Met Arg Glu Gly Pro Ala Lys Asn Met Val Lys Gln Lys Ala Leu Arg

55

60

65

gtt tta aag caa aag agg atg tat gag cag cag cgg gac aat ctt gcc 297
 Val Leu Lys Gln Lys Arg Met Tyr Glu Gln Gln Arg Asp Asn Leu Ala

70

75

80

caa cag tca ttc aac atg gaa caa gcc aat tat acc atc cag tct ttg 345
 Gln Gln Ser Phe Asn Met Glu Gln Ala Asn Tyr Thr Ile Gln Ser Leu

85

90

95

aag gac acc aag acc acg gtt gat gct atg aaa ctg gga gta aag gaa 393
 Lys Asp Thr Lys Thr Thr Val Asp Ala Met Lys Leu Gly Val Lys Glu

100

105

110

115

atg aag aag gca tac aag caa gtg aag atc gac cag att gag gat tta 441

Met Lys Lys Ala Tyr Lys Gln Val Lys Ile Asp Gln Ile Glu Asp Leu
 120 125 130

caa gac cag cta gag gat atg atg gaa gat gca aat gaa atc caa gaa 489
 Gln Asp Gln Leu Glu Asp Met Met Glu Asp Ala Asn Glu Ile Gln Glu
 135 140 145

gca ctg agt cgc agt tat ggc acc cca gaa ctg gat gaa gat gat tta 537
 Ala Leu Ser Arg Ser Tyr Gly Thr Pro Glu Leu Asp Glu Asp Asp Leu
 150 155 160

gaa gca gag ttg gat gca cta ggt gat gag ctt ctg gct gat gaa gac 585
 Glu Ala Glu Leu Asp Ala Leu Gly Asp Glu Leu Leu Ala Asp Glu Asp
 165 170 175

agt tct tat ttg gat gag gca gca tct gca cct gca att cca gaa ggt 633
 Ser Ser Tyr Leu Asp Glu Ala Ala Ser Ala Pro Ala Ile Pro Glu Gly
 180 185 190 195

gtt ccc act gat aca aaa aac aag gat gga gtt ctg gtg gat gaa ttt 681
 Val Pro Thr Asp Thr Lys Asn Lys Asp Gly Val Leu Val Asp Glu Phe
 200 205 210

gga ttg cca cag atc cct gct tca tagatttgca tcattcaagc atatcttgta 735
 Gly Leu Pro Gln Ile Pro Ala Ser
 215

aaacaaacac atattatggg actaggaaat atttattcttt ccaaatttgc cataacagat 795

ttaggtttct ttcctttctt tgaaggaaag ttttaattaca ttgccttttt attttttcca 855
 ttaagagact cattgcttgg gaaatgcctt cttegtacta aaatttgatt cctttttttt 915
 cttatgaaaa acgaactcag tttaaaagta tttttagctc gtatgacttg ttttcattca 975
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 ctctacagtc tcaaaatgac ctgataaatt gataagacaa agatgagatt attggggctg 1095
 ttcatattat gattcagaat cattttctat tgttgtatta taggttggtt aaagtgatgg 1155
 cctttttgat gggttttggt gtgtcttgtg aacaagtcgt tactgtgtcc attattggaa 1215
 tggaattatc actactgtat catgagtggg tattttgatt ctatggttcc ctcagtatta 1275
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 tatactcaat aaatatTTTT caaaagg 1362

<210> 63

<211> 622

<212> PRT

<213> Homo sapiens

<400> 63

Met Ala Asp Gly Pro Asp Glu Tyr Asp Thr Glu Ala Gly Cys Val Pro

1

5

10

15

Leu Leu His Pro Glu Glu Ile Lys Pro Gln Ser His Tyr Asn His Gly

20

25

30

Tyr Gly Glu Pro Leu Gly Arg Lys Thr His Ile Asp Asp Tyr Ser Thr

35

40

45

Trp Asp Ile Val Lys Ala Thr Gln Tyr Gly Ile Tyr Glu Arg Cys Arg

50

55

60

Glu Leu Val Glu Ala Gly Tyr Asp Val Arg Gln Pro Asp Lys Glu Asn

65

70

75

80

Val Thr Leu Leu His Trp Ala Ala Ile Asn Asn Arg Ile Asp Leu Val

85

90

95

Lys Tyr Tyr Ile Ser Lys Gly Ala Ile Val Asp Gln Leu Gly Gly Asp

100

105

110

Leu Asn Ser Thr Pro Leu His Trp Ala Thr Arg Gln Gly His Leu Ser

115

120

125

Met Val Val Gln Leu Met Lys Tyr Gly Ala Asp Pro Ser Leu Ile Asp

130

135

140

Gly Glu Gly Cys Ser Cys Ile His Leu Ala Ala Gln Phe Gly His Thr

145

150

155

160

Ser Ile Val Ala Tyr Leu Ile Ala Lys Gly Gln Asp Val Asp Met Met

165

170

175

Asp Gln Asn Gly Met Thr Pro Leu Met Trp Ala Ala Tyr Arg Thr His

180

185

190

Ser Val Asp Pro Thr Arg Leu Leu Leu Thr Phe Asn Val Ser Val Asn

195

200

205

Leu Gly Asp Lys Tyr His Lys Asn Thr Ala Leu His Trp Ala Val Leu

210

215

220

Ala Gly Asn Thr Thr Val Ile Ser Leu Leu Leu Glu Ala Gly Ala Asn

225

230

235

240

Val Asp Ala Gln Asn Ile Lys Gly Glu Ser Ala Leu Asp Leu Ala Lys

245

250

255

Gln Arg Lys Asn Val Trp Met Ile Asn His Leu Gln Glu Ala Arg Gln

260

265

270

Ala Lys Gly Tyr Asp Asn Pro Ser Phe Leu Arg Lys Leu Lys Ala Asp

275

280

285

Lys Glu Phe Arg Gln Lys Val Met Leu Gly Thr Pro Phe Leu Val Ile

290

295

300

Trp Leu Val Gly Phe Ile Ala Asp Leu Asn Ile Asp Ser Trp Leu Ile

305

310

315

320

Lys Gly Leu Met Tyr Gly Gly Val Trp Ala Thr Val Gln Phe Leu Ser
325 330 335

Lys Ser Phe Phe Asp His Ser Met His Ser Ala Leu Pro Leu Gly Ile
340 345 350

Tyr Leu Ala Thr Lys Phe Trp Met Tyr Val Thr Trp Phe Phe Trp Phe
355 360 365

Trp Asn Asp Leu Asn Phe Leu Phe Ile His Leu Pro Phe Leu Ala Asn
370 375 380

Ser Val Ala Leu Phe Tyr Asn Phe Gly Lys Ser Trp Lys Ser Asp Pro
385 390 395 400

Gly Ile Ile Lys Ala Thr Glu Glu Gln Lys Lys Lys Thr Ile Val Glu
405 410 415

Leu Ala Glu Thr Gly Ser Leu Asp Leu Ser Ile Phe Cys Ser Thr Cys
420 425 430

Leu Ile Arg Lys Pro Val Arg Ser Lys His Cys Gly Val Cys Asn Arg
435 440 445

Cys Ile Ala Lys Phe Asp His His Cys Pro Trp Val Gly Asn Cys Val
450 455 460

Gly Ala Gly Asn His Arg Tyr Phe Met Gly Tyr Leu Phe Phe Leu Leu
465 470 475 480

Phe Met Ile Cys Trp Met Ile Tyr Gly Cys Ile Ser Tyr Trp Gly Leu
485 490 495

His Cys Glu Thr Thr Tyr Thr Lys Asp Gly Phe Trp Thr Tyr Ile Thr
500 505 510

Gln Ile Ala Thr Cys Ser Pro Trp Met Phe Trp Met Phe Leu Asn Ser
515 520 525

Val Phe His Phe Met Trp Val Ala Val Leu Leu Met Cys Gln Met Tyr
530 535 540

Gln Ile Ser Cys Leu Gly Ile Thr Thr Asn Glu Arg Met Asn Ala Arg
545 550 555 560

Arg Tyr Lys His Phe Lys Val Thr Thr Thr Ser Ile Glu Ser Pro Phe
565 570 575

Asn His Gly Cys Val Arg Asn Ile Ile Asp Phe Phe Glu Phe Arg Cys
580 585 590

Cys Gly Leu Phe Arg Pro Val Ile Val Asp Trp Thr Arg Gln Tyr Thr
595 600 605

Ile Glu Tyr Asp Gln Ile Ser Gly Ser Gly Tyr Gln Leu Val
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<210> 64

<211> 2948

<212> DNA

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<222> (14).. (1879)

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 Met Ala Asp Gly Pro Asp Glu Tyr Asp Thr Glu Ala
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ggc tgt gtg ccc ctt ctc cac cca gag gaa atc aaa ccc caa agc cat 97
 Gly Cys Val Pro Leu Leu His Pro Glu Glu Ile Lys Pro Gln Ser His
 15 20 25

tat aac cat gga tat ggt gaa cct ctt gga cgg aaa act cat att gat 145
 Tyr Asn His Gly Tyr Gly Glu Pro Leu Gly Arg Lys Thr His Ile Asp
 30 35 40

gat tac agc aca tgg gac ata gtc aag gct aca caa tat gga ata tat 193
 Asp Tyr Ser Thr Trp Asp Ile Val Lys Ala Thr Gln Tyr Gly Ile Tyr
 45 50 55 60

gaa cgc tgt cga gaa ttg gtg gaa gca ggt tat gat gta cgg caa ccg 241
 Glu Arg Cys Arg Glu Leu Val Glu Ala Gly Tyr Asp Val Arg Gln Pro
 65 70 75

gac aaa gaa aat gtt acc ctc ctc cat tgg gct gcc atc aat aac aga 289

Asp Lys Glu Asn Val Thr Leu Leu His Trp Ala Ala Ile Asn Asn Arg

80

85

90

ata gat tta gtc aaa tac tat att tcg aaa ggt gct att gtg gat caa 337

Ile Asp Leu Val Lys Tyr Tyr Ile Ser Lys Gly Ala Ile Val Asp Gln

95

100

105

ctt gga ggg gac ctg aat tca act cca ttg cac tgg gcc aca aga caa 385

Leu Gly Gly Asp Leu Asn Ser Thr Pro Leu His Trp Ala Thr Arg Gln

110

115

120

ggc cat cta tcc atg gtt gtg caa cta atg aaa tat ggt gca gat cct 433

Gly His Leu Ser Met Val Val Gln Leu Met Lys Tyr Gly Ala Asp Pro

125

130

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tca tta att gat gga gaa gga tgt agc tgt att cat ctg gct gct cag 481

Ser Leu Ile Asp Gly Glu Gly Cys Ser Cys Ile His Leu Ala Ala Gln

145

150

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ttc gga cat acc tca att gtt gct tat ctc ata gca aaa gga cag gat 529

Phe Gly His Thr Ser Ile Val Ala Tyr Leu Ile Ala Lys Gly Gln Asp

160

165

170

gta gat atg atg gat cag aat gga atg acg cct tta atg tgg gca gca 577

Val Asp Met Met Asp Gln Asn Gly Met Thr Pro Leu Met Trp Ala Ala

175

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185

tat aga aca cat agt gtg gat cca act aga ttg ctt tta aca ttc aat 625
 Tyr Arg Thr His Ser Val Asp Pro Thr Arg Leu Leu Leu Thr Phe Asn
 190 195 200

gtt tca gtt aac ctt ggt gac aag tat cac aaa aac act gct ctg cat 673
 Val Ser Val Asn Leu Gly Asp Lys Tyr His Lys Asn Thr Ala Leu His
 205 210 215 220

tgg gca gtg cia gca ggg aat acc aca gtc att agc ctt ctt ctg gaa 721
 Trp Ala Val Leu Ala Gly Asn Thr Thr Val Ile Ser Leu Leu Leu Glu
 225 230 235

gct gga gct aat gtt gat gcc cag aat atc aag ggc gaa tca gcg ctt 769
 Ala Gly Ala Asn Val Asp Ala Gln Asn Ile Lys Gly Glu Ser Ala Leu
 240 245 250

gat ttg gca aaa cag aga aaa aat gtg tgg atg atc aac cac tta caa 817
 Asp Leu Ala Lys Gln Arg Lys Asn Val Trp Met Ile Asn His Leu Gln
 255 260 265

gag gca agg caa gca aaa gga tat gac aat ccg tcc ttc ctt aga aag 865
 Glu Ala Arg Gln Ala Lys Gly Tyr Asp Asn Pro Ser Phe Leu Arg Lys
 270 275 280

ctg aaa gct gat aag gaa ttt cgg cag aaa gta atg tta gga act cct 913
 Leu Lys Ala Asp Lys Glu Phe Arg Gln Lys Val Met Leu Gly Thr Pro
 285 290 295 300

ttc cta gtt att tgg ctg gtt ggg ttt ata gca gac cta aat att gat 961

Phe Leu Val Ile Trp Leu Val Gly Phe Ile Ala Asp Leu Asn Ile Asp

305

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tct tgg ctc att aaa ggg cta atg tat ggt ggt gtt tgg gct aca gta 1009

Ser Trp Leu Ile Lys Gly Leu Met Tyr Gly Gly Val Trp Ala Thr Val

320

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cag ttt ctt tca aaa tcc ttt ttc gat cat tca atg cat agt gca ttg 1057

Gln Phe Leu Ser Lys Ser Phe Phe Asp His Ser Met His Ser Ala Leu

335

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ccc ctt ggg ata tat ttg gca acc aaa ttc tgg atg tat gtg acg tgg 1105

Pro Leu Gly Ile Tyr Leu Ala Thr Lys Phe Trp Met Tyr Val Thr Trp

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ttc ttc tgg ttt tgg aat gat ctc aac ttt tta ttt atc cat ctt cca 1153

Phe Phe Trp Phe Trp Asn Asp Leu Asn Phe Leu Phe Ile His Leu Pro

365

370

375

380

ttc ctt gcc aat agt gtt gca ctt ttc tac aat ttt gga aaa tct tgg 1201

Phe Leu Ala Asn Ser Val Ala Leu Phe Tyr Asn Phe Gly Lys Ser Trp

385

390

395

aaa tca gat cca ggg att att aaa gca aca gaa gag caa aag aaa aag 1249

Lys Ser Asp Pro Gly Ile Ile Lys Ala Thr Glu Glu Gln Lys Lys Lys

400

405

410

aca ata gtt gaa ctt gca gag aca gga agt ctg gac ctc agt ata ttc 1297

Thr Ile Val Glu Leu Ala Glu Thr Gly Ser Leu Asp Leu Ser Ile Phe

415	420	425	
tgc agt acc tgt ttg ata cga aaa ccg gtg agg tcc aaa cat tgt ggt	1345		
Cys Ser Thr Cys Leu Ile Arg Lys Pro Val Arg Ser Lys His Cys Gly			
430	435	440	
gtg tgc aac cgc tgt ata gca aaa ttt gat cat cat tgc cca tgg gtg	1393		
Val Cys Asn Arg Cys Ile Ala Lys Phe Asp His His Cys Pro Trp Val			
445	450	455	460
ggc aac tgt gta ggt gca ggc aac cat aga tat ttt atg ggc tac cta	1441		
Gly Asn Cys Val Gly Ala Gly Asn His Arg Tyr Phe Met Gly Tyr Leu			
465	470	475	
ttc ttc ttg ctt ttt atg atc tgc tgg atg att tat ggt tgt ata tct	1489		
Phe Phe Leu Leu Phe Met Ile Cys Trp Met Ile Tyr Gly Cys Ile Ser			
480	485	490	
tac tgg gga ctc cac tgt gag acc act tac acc aag gat gga ttt tgg	1537		
Tyr Trp Gly Leu His Cys Glu Thr Thr Tyr Thr Lys Asp Gly Phe Trp			
495	500	505	
aca tac att act cag att gcc acg tgt tca cct tgg atg ttt tgg atg	1585		
Thr Tyr Ile Thr Gln Ile Ala Thr Cys Ser Pro Trp Met Phe Trp Met			
510	515	520	
ttc ctg aac agt gtt ttc cac ttc atg tgg gtg gct gta tta ctc atg	1633		
Phe Leu Asn Ser Val Phe His Phe Met Trp Val Ala Val Leu Leu Met			
525	530	535	540

tgt cag atg tac cag ata tca tgt tta ggt att act aca aat gaa aga 1681

Cys Gln Met Tyr Gln Ile Ser Cys Leu Gly Ile Thr Thr Asn Glu Arg

545

550

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atg aat gcc agg aga tac aag cac ttt aaa gtc aca aca acg tct att 1729

Met Asn Ala Arg Arg Tyr Lys His Phe Lys Val Thr Thr Thr Ser Ile

560

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570

gaa agc cca ttc aac cat gga tgt gta aga aat att ata gac ttc ttt 1777

Glu Ser Pro Phe Asn His Gly Cys Val Arg Asn Ile Ile Asp Phe Phe

575

580

585

gaa ttt cga tgc tgt ggc ctc ttt cgt cct gtt atc gtg gac tgg acc 1825

Glu Phe Arg Cys Cys Gly Leu Phe Arg Pro Val Ile Val Asp Trp Thr

590

595

600

agg cag tat aca ata gaa tat gac caa ata tca gga tct ggg tac cag 1873

Arg Gln Tyr Thr Ile Glu Tyr Asp Gln Ile Ser Gly Ser Gly Tyr Gln

605

610

615

620

ctg gtg tagcgacatc ttatcctaig aagcatattg ctgagtggcg cctgaaaatt 1929

Leu Val

gtgtctgtcc gtgtctttct cacactcgaa tccacatcct ttgaacaaga gcatgctatg 1989

tglagggcta atggatgaatt ttacagtctt tttttcaaca cttttattaa caaaagtaaa 2049

catggacaga acacacigcc atttctggga agagtaaaga tgataaaaaa taattttaat 2109

ggttcttaat gtggaaattc acaacatact caacttttgg gttttgttct cacagtattt 2169
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taatagtgat acatggatat acttccittt aaattctcag ctgcaaaata attgtagaca 2829
aaataatggc atttaactaa agatggagca tgatctgtgt acatagcaca tgtgaataaa 2889
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<210> 65

<211> 632

<212> PRT

<213> Homo sapiens

<400> 65

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15

Glu Tyr Asp Thr Glu Ala Gly Cys Val Pro Leu Leu His Pro Glu Glu

20

25

30

Ile Lys Pro Gln Ser His Tyr Asn His Gly Tyr Gly Glu Pro Leu Gly

35

40

45

Arg Lys Thr His Ile Asp Asp Tyr Ser Thr Trp Asp Ile Val Lys Ala

50

55

60

Thr Gln Tyr Gly Ile Tyr Glu Arg Cys Arg Glu Leu Val Glu Ala Gly

65

70

75

80

Tyr Asp Val Arg Gln Pro Asp Lys Glu Asn Val Thr Leu Leu His Trp

85

90

95

Ala Ala Ile Asn Asn Arg Ile Asp Leu Val Lys Tyr Tyr Ile Ser Lys

100

105

110

Gly Ala Ile Val Asp Gln Leu Gly Gly Asp Leu Asn Ser Thr Pro Leu

115

120

125

His Trp Ala Thr Arg Gln Gly His Leu Ser Met Val Val Gln Leu Met

130

135

140

Lys Tyr Gly Ala Asp Pro Ser Leu Ile Asp Gly Glu Gly Cys Ser Cys

145

150

155

160

Ile His Leu Ala Ala Gln Phe Gly His Thr Ser Ile Val Ala Tyr Leu

165

170

175

Ile Ala Lys Gly Gln Asp Val Asp Met Met Asp Gln Asn Gly Met Thr

180

185

190

Pro Leu Met Trp Ala Ala Tyr Arg Thr His Ser Val Asp Pro Thr Arg

195

200

205

Leu Leu Leu Thr Phe Asn Val Ser Val Asn Leu Gly Asp Lys Tyr His

210

215

220

Lys Asn Thr Ala Leu His Trp Ala Val Leu Ala Gly Asn Thr Thr Val

225

230

235

240

Ile Ser Leu Leu Leu Glu Ala Gly Ala Asn Val Asp Ala Gln Asn Ile

245

250

255

Lys Gly Glu Ser Ala Leu Asp Leu Ala Lys Gln Arg Lys Asn Val Trp

260

265

270

Met Ile Asn His Leu Gln Glu Ala Arg Gln Ala Lys Gly Tyr Asp Asn
275 280 285

Pro Ser Phe Leu Arg Lys Leu Lys Ala Asp Lys Glu Phe Arg Gln Lys
290 295 300

Val Met Leu Gly Thr Pro Phe Leu Val Ile Trp Leu Val Gly Phe Ile
305 310 315 320

Ala Asp Leu Asn Ile Asp Ser Trp Leu Ile Lys Gly Leu Met Tyr Gly
325 330 335

Gly Val Trp Ala Thr Val Gln Phe Leu Ser Lys Ser Phe Phe Asp His
340 345 350

Ser Met His Ser Ala Leu Pro Leu Gly Ile Tyr Leu Ala Thr Lys Phe
355 360 365

Trp Met Tyr Val Thr Trp Phe Phe Trp Phe Trp Asn Asp Leu Asn Phe
370 375 380

Leu Phe Ile His Leu Pro Phe Leu Ala Asn Ser Val Ala Leu Phe Tyr
385 390 395 400

Asn Phe Gly Lys Ser Trp Lys Ser Asp Pro Gly Ile Ile Lys Ala Thr
405 410 415

Glu Glu Gln Lys Lys Lys Thr Ile Val Glu Leu Ala Glu Thr Gly Ser
420 425 430

Leu Asp Leu Ser Ile Phe Cys Ser Thr Cys Leu Ile Arg Lys Pro Val

435

440

445

Arg Ser Lys His Cys Gly Val Cys Asn Arg Cys Ile Ala Lys Phe Asp

450

455

460

His His Cys Pro Trp Val Gly Asn Cys Val Gly Ala Gly Asn His Arg

465

470

475

480

Tyr Phe Met Gly Tyr Leu Phe Phe Leu Leu Phe Met Ile Cys Trp Met

485

490

495

Ile Tyr Gly Cys Ile Ser Tyr Trp Gly Leu His Cys Glu Thr Thr Tyr

500

505

510

Thr Lys Asp Gly Phe Trp Thr Tyr Ile Thr Gln Ile Ala Thr Cys Ser

515

520

525

Pro Trp Met Phe Trp Met Phe Leu Asn Ser Val Phe His Phe Met Trp

530

535

540

Val Ala Val Leu Leu Met Cys Gln Met Tyr Gln Ile Ser Cys Leu Gly

545

550

555

560

Ile Thr Thr Asn Glu Arg Met Asn Ala Arg Arg Tyr Lys His Phe Lys

565

570

575

Val Thr Thr Thr Ser Ile Glu Ser Pro Phe Asn His Gly Cys Val Arg

580

585

590

Asn Ile Ile Asp Phe Phe Glu Phe Arg Cys Cys Gly Leu Phe Arg Pro
595 600 605

Val Ile Val Asp Trp Thr Arg Gln Tyr Thr Ile Glu Tyr Asp Gln Ile
610 615 620

Ser Gly Ser Gly Tyr Gln Leu Val
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<210> 66

<211> 4715

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> (108).. (2003)

<400> 66

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cctccgcctc gcccgagccc cgggagggcg aaacgcttc tcccagc atg cag cgg 116

Met Gln Arg

1

gag gag gga ttt aac acc aag atg gcg gac ggc ccg gat gag tac gat 164

Glu Glu Gly Phe Asn Thr Lys Met Ala Asp Gly Pro Asp Glu Tyr Asp

5

10

15

acc gaa gcg ggc tgt gtg ccc ctt ctc cac cca gag gaa atc aaa ccc 212

Thr Glu Ala Gly Cys Val Pro Leu Leu His Pro Glu Glu Ile Lys Pro

20

25

30

35

caa agc cat tat aac cat gga tat ggt gaa cct ctt gga cgg aaa act 260

Gln Ser His Tyr Asn His Gly Tyr Gly Glu Pro Leu Gly Arg Lys Thr

40

45

50

cat att gat gat tac agc aca tgg gac ata gtc aag gct aca caa tat 308

His Ile Asp Asp Tyr Ser Thr Trp Asp Ile Val Lys Ala Thr Gln Tyr

55

60

65

gga ata tat gaa cgc tgt cga gaa ttg gtg gaa gca ggt tat gat gta 356

Gly Ile Tyr Glu Arg Cys Arg Glu Leu Val Glu Ala Gly Tyr Asp Val

70

75

80

cgg caa ccg gac aaa gaa aat gtt acc ctc ctc cat tgg gct gcc atc 404

Arg Gln Pro Asp Lys Glu Asn Val Thr Leu Leu His Trp Ala Ala Ile

85

90

95

aat aac aga ata gat tta gtc aaa tac tat att tcg aaa ggt gct att 452

Asn Asn Arg Ile Asp Leu Val Lys Tyr Tyr Ile Ser Lys Gly Ala Ile

100

105

110

115

gtg gat caa ctt gga ggg gac ctg aat tca act cca ttg cac tgg gcc 500

Val Asp Gln Leu Gly Gly Asp Leu Asn Ser Thr Pro Leu His Trp Ala

120

125

130

aca aga caa ggc cat cta tcc atg gtt gtg caa cta atg aaa tat ggt 548

Thr Arg Gln Gly His Leu Ser Met Val Val Gln Leu Met Lys Tyr Gly

135

140

145

gca gat cct tca tta att gat gga gaa gga tgt agc tgt att cat ctg 596

Ala Asp Pro Ser Leu Ile Asp Gly Glu Gly Cys Ser Cys Ile His Leu

150

155

160

gct gct cag ttc gga cat acc tca att gtt gct tat ctc ata gca aaa 644

Ala Ala Gln Phe Gly His Thr Ser Ile Val Ala Tyr Leu Ile Ala Lys

165

170

175

gga cag gat gta gat atg atg gat cag aat gga atg acg cct tta atg 692

Gly Gln Asp Val Asp Met Met Asp Gln Asn Gly Met Thr Pro Leu Met

180

185

190

195

tgg gca gca tat aga aca cat agt gtg gat cca act aga ttg ctt tta 740

Trp Ala Ala Tyr Arg Thr His Ser Val Asp Pro Thr Arg Leu Leu Leu

200

205

210

aca ttc aat gtt tca gtt aac ctt ggt gac aag tat cac aaa aac act 788

Thr Phe Asn Val Ser Val Asn Leu Gly Asp Lys Tyr His Lys Asn Thr

215

220

225

gct ctg cat tgg gca gtg cta gca ggg aat acc aca gtc att agc ctt 836

Ala Leu His Trp Ala Val Leu Ala Gly Asn Thr Thr Val Ile Ser Leu

230

235

240

ctt ctg gaa gct gga gct aat gtt gat gcc cag aat atc aag ggc gaa 884

Leu Leu Glu Ala Gly Ala Asn Val Asp Ala Gln Asn Ile Lys Gly Glu

245

250

255

tca gcg ctt gat ttg gca aaa cag aga aaa aat gtg tgg atg atc aac 932

Ser Ala Leu Asp Leu Ala Lys Gln Arg Lys Asn Val Trp Met Ile Asn

260

265

270

275

cac tta caa gag gca agg caa gca aaa gga tat gac aat ccg tcc ttc 980

His Leu Gln Glu Ala Arg Gln Ala Lys Gly Tyr Asp Asn Pro Ser Phe

280

285

290

ctt aga aag ctg aaa gct gat aag gaa ttt cgg cag aaa gta atg tta 1028

Leu Arg Lys Leu Lys Ala Asp Lys Glu Phe Arg Gln Lys Val Met Leu

295

300

305

gga act cct ttc cta gtt att tgg ctg gtt ggg ttt ata gca gac cta 1076

Gly Thr Pro Phe Leu Val Ile Trp Leu Val Gly Phe Ile Ala Asp Leu

310

315

320

aat att gat tct tgg ctc att aaa ggg cta atg tat ggt ggt gtt tgg 1124

Asn Ile Asp Ser Trp Leu Ile Lys Gly Leu Met Tyr Gly Gly Val Trp

325

330

335

gct aca gta cag ttt ctt tca aaa tcc ttt ttc gat cat tca atg cat 1172

Ala Thr Val Gln Phe Leu Ser Lys Ser Phe Phe Asp His Ser Met His

340

345

350

355

agt gca ttg ccc ctt ggg ata tat ttg gca acc aaa ttc tgg atg tat 1220
 Ser Ala Leu Pro Leu Gly Ile Tyr Leu Ala Thr Lys Phe Trp Met Tyr

360

365

370

gtg acg tgg ttc ttc tgg ttt tgg aat gat ctc aac ttt tta ttt atc 1268
 Val Thr Trp Phe Phe Trp Phe Trp Asn Asp Leu Asn Phe Leu Phe Ile

375

380

385

cat ctt cca ttc ctt gcc aat agt gtt gca ctt ttc tac aat ttt gga 1316
 His Leu Pro Phe Leu Ala Asn Ser Val Ala Leu Phe Tyr Asn Phe Gly

390

395

400

aaa tct tgg aaa tca gat cca ggg att att aaa gca aca gaa gag caa 1364
 Lys Ser Trp Lys Ser Asp Pro Gly Ile Ile Lys Ala Thr Glu Glu Gln

405

410

415

aag aaa aag aca ata gtt gaa ctt gca gag aca gga agt ctg gac ctc 1412
 Lys Lys Lys Thr Ile Val Glu Leu Ala Glu Thr Gly Ser Leu Asp Leu

420

425

430

435

agt ata ttc tgc agt acc tgt ttg ata cga aaa ccg gtg agg tcc aaa 1460
 Ser Ile Phe Cys Ser Thr Cys Leu Ile Arg Lys Pro Val Arg Ser Lys

440

445

450

cat tgt ggt gtg tgc aac cgc tgt ata gca aaa ttt gat cat cat tgc 1508
 His Cys Gly Val Cys Asn Arg Cys Ile Ala Lys Phe Asp His His Cys

455

460

465

cca tgg gtg ggt aac tgt gta ggt gca ggc aac cat aga tat ttt atg 1556

Pro Trp Val Gly Asn Cys Val Gly Ala Gly Asn His Arg Tyr Phe Met

470

475

480

ggc tac cta ttc ttc ttg ctt ttt atg atc tgc tgg atg att tat ggt 1604

Gly Tyr Leu Phe Phe Leu Leu Phe Met Ile Cys Trp Met Ile Tyr Gly

485

490

495

tgt ata tct tac tgg gga ctc cac tgt gag acc act tac acc aag gat 1652

Cys Ile Ser Tyr Trp Gly Leu His Cys Glu Thr Thr Tyr Thr Lys Asp

500

505

510

515

gga ttt tgg aca tac att act cag att gcc acg tgt tca cct tgg atg 1700

Gly Phe Trp Thr Tyr Ile Thr Gln Ile Ala Thr Cys Ser Pro Trp Met

520

525

530

ttt tgg atg ttc ctg aac agt gtt ttc cac ttc atg tgg gtg gct gta 1748

Phe Trp Met Phe Leu Asn Ser Val Phe His Phe Met Trp Val Ala Val

535

540

545

tta ctc atg tgt cag atg tac cag ata tca tgt tta ggt att act aca 1796

Leu Leu Met Cys Gln Met Tyr Gln Ile Ser Cys Leu Gly Ile Thr Thr

550

555

560

aat gaa aga atg aat gcc agg aga tac aag cac ttt aaa gtc aca aca 1844

Asn Glu Arg Met Asn Ala Arg Arg Tyr Lys His Phe Lys Val Thr Thr

565

570

575

acg tct att gaa agc cca ttc aac cat gga tgt gta aga aat att ata 1892

Thr Ser Ile Glu Ser Pro Phe Asn His Gly Cys Val Arg Asn Ile Ile

580

585

590

595

gac ttc ttt gaa ttt cga tgc tgt ggc ctc ttt cgt cct gtt atc gtg 1940

Asp Phe Phe Glu Phe Arg Cys Cys Gly Leu Phe Arg Pro Val Ile Val

600

605

610

gac tgg acc agg cag tat aca ata gaa tat gac caa ata tca gga tct 1988

Asp Trp Thr Arg Gln Tyr Thr Ile Glu Tyr Asp Gln Ile Ser Gly Ser

615

620

625

ggg tac cag ctg gtg tagcgacatc ttatcctatg aagcatattg ctgagtggcg 2043

Gly Tyr Gln Leu Val

630

cctgaaaatt gtgtctgtcc gtgtctttct cacactcgaa tccacatcct ttgaacaaga 2103

gcatgctatg tgtagggcta atgggtgaatt ttacagtcct tttttcaaca cttttattaa 2163

caaaagtaaa catggacaga acacactgcc atttctggga agagtaaaga tgataaaaaa 2223

taattttaat ggttcttaat gtggaaattc acaacatact caacttttgg gttttgttct 2283

cacagtattt ttacaaaaa aagggttaaac ttattctatt gacagacatg gtgtactgat 2343

cagaaatgtt cagttttaac taaaactaaa ttatggtat ttggctaaat gttatgatgc 2403

agtctagtac gagtattgca tctaattcca ggagcattgt ttttaagttga ttgactagtt 2463

attaigtaca tticagaatg tacacataaa tactgtgatg aaaatcatgt gattgggatc 2523

tactgtgatg ttgtcttcaa aggcaggaga aaataatgtt cacaataaaa tgtgctaaca 2583
atgttttgtt tctatcagct gtgcaatgc tgatatattt ctagttcagt gaaataattt 2643
gtagtaacct tactctgagg ttttacggtc tgataatgaa gcacttgcct gagtatagta 2703
agtcagtgtt ttttgttcaa atttaaaagc cctgctaatt gcatgacaca ccacatagaa 2763
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aaattctcag taatagtgt acatggatat acttcccttt aaattctcag ctgcaaaata 2943
attgtagaca aaataatggc atttaactaa agatggagca tgatctaagt acatagcaca 3003
tgtgaataaa agaaaagctg acagtatatt ctggtttcaa taaaatgacc tatcagaaag 3063
tagaatttca tccccaagag tatttcagtt tatccaatat tgagtaagtt ctgaaacagt 3123
tttagaaaaa attttctttt tgttaaagt gatgcactga tcaatttttg tcacagcatt 3183
ttcataccit catggtggac tactagtcac tgcttcata aatattgttt acagggtgag 3243
atttggttta ttaactttaa gtgctgtagc aaactgtggt tcgagcaacc tgtgggaaat 3303
ctgtgagagg gaatgggtg ggagatgtg gggaatggtg gtcagactga tgacagatcc 3363

tagaccaatg taaagaatgt gtatctgtat ataaataatt tatcaaatag ttttctcttt 3423

gtgtctgtgt tagtgttttt aaagctgctc atttcatttt gtccaaccaa aaagaaaagg 3483

gagataacta atgagcttct agtgatgttc aaaattgctg ttaataggca ttataccctg 3543

caagttcact gcatgtctga tgcttggtaa aactagtctt cctgtaaaa tgcagattac 3603

aggtattaaa gcaatctagt ggtatacccg ccccttgcct tagtaagagg agcagtgaag 3663

tgtatatagt tgatgttcag tatttccaag taccattttt atatagtagc ttatttgacc 3723

ataagtcaca catcaaaaaa agattaccct tagtgtatgt gttttaatat tagaaaattg 3783

gcatatgtac tttatttttg aaaagggaag agatgggtgt ggggtggcaa tagcattgtg 3843

ccattttgtc atagaatgta aaaattggtt aactttacaa atgtcagcta gttttgacta 3903

ctaattgggg gaaattttag ataattttta aattcaaagt tatttataaa atgctagaat 3963

ttgttttaat tttttgtatt ttgagccact tcacatgaag actcagttgc atttttatcg 4023

aatacatttt tatcaacagt taaagactat ggtgggtttt tcagagtttg gctaagaatg 4083

ttgttaccat ctcttttgtt tgtggtacaa tattttcagt gcaaaagaga tgtcattcag 4143

ttaaaaagac aaacctctag atgtgttaatt acatggaaaa tactagcaat gtgaatgctt 4203

ttgtagtaac catctttag tagctgtgaa atctataact cagaaatggt cagatggtea 4263

ggagccagct atgcagcagt ataccatctg ttttaattatt ttgtaggtcc tgtgtgtgga 4323

accaactata aaccagttc taaagtgtg tatgatggg aacctttggg aatagttctt 4383

atcaacttaa ttggatactt ttagcaaata ggaacttaat tctcagcact gaacatgaat 4443

tacttccitg gagttttttt tcattcatat ttttgttgtt tccaggaatt tatttgatat 4503

taatgggctg aaaacagcat cattgtactt aagctatgga tgtttttatt ttatatattc 4563

tttatattata actgtgccaa gtattatttt gctacttacc gtgttattct gtggaaagaa 4623

aaacctgtaa agtgtttaat aaattagccc tccttacata aattaaatgt caaaattttg 4683

taaaatatta atcagaataa atactgactc tt 4715

<210> 67

<211> 498

<212> PRT

<213> Homo sapiens

<400> 67

Met Ala Arg Leu Glu Val Ile Glu Leu Pro His Ser Pro Gln Asn Leu

1

5

10

15

Leu Val Ser Pro Asn Ser Ser His Ser His Ala Val Val Leu Ser Trp

20

25

30

Val Arg Pro Phe Asp Gly Asn Ser Pro Ile Leu Tyr Tyr Ile Val Glu

35

40

45

Leu Ser Glu Asn Asn Ser Pro Trp Lys Val His Leu Ser Asn Val Gly

50

55

60

Pro Glu Met Thr Gly Val Thr Val Ser Gly Leu Thr Pro Ala Arg Thr

65

70

75

80

Tyr Gln Phe Arg Val Cys Ala Val Asn Glu Val Gly Arg Gly Gln Tyr

85

90

95

Ser Ala Glu Thr Ser Arg Leu Met Leu Pro Glu Glu Pro Pro Ser Ala

100

105

110

Pro Pro Lys Asn Ile Val Ala Ser Gly Arg Thr Asn Gln Ser Ile Met

115

120

125

Val Gln Trp Gln Pro Pro Pro Glu Thr Glu His Asn Gly Val Leu Arg

130

135

140

Gly Tyr Ile Leu Arg Tyr Arg Leu Ala Gly Leu Pro Gly Glu Tyr Gln

145

150

155

160

Gln Arg Asn Ile Thr Ser Pro Glu Val Asn Tyr Cys Leu Val Thr Asp

165

170

175

Leu Ile Ile Trp Thr Gln Tyr Glu Ile Gln Val Ala Ala Tyr Asn Gly

180

185

190

Ala Gly Leu Gly Val Phe Ser Arg Ala Val Thr Glu Tyr Thr Leu Gln

195

200

205

Gly Val Pro Thr Ala Pro Pro Gln Asn Val Gln Thr Glu Ala Val Asn

210

215

220

Ser Thr Thr Ile Gln Phe Leu Trp Asn Pro Pro Pro Gln Gln Phe Ile

225

230

235

240

Asn Gly Ile Asn Gln Gly Tyr Lys Leu Leu Ala Trp Pro Ala Asp Ala

245

250

255

Pro Glu Ala Val Thr Val Val Thr Ile Ala Pro Asp Phe His Gly Val

260

265

270

His His Gly His Ile Thr Asn Leu Lys Lys Phe Thr Ala Tyr Phe Thr

275

280

285

Ser Val Leu Cys Phe Thr Thr Pro Gly Asp Gly Pro Pro Ser Thr Pro

290

295

300

Gln Leu Val Trp Thr Gln Glu Asp Lys Pro Gly Ala Val Gly His Leu

305

310

315

320

Ser Phe Thr Glu Ile Leu Asp Thr Ser Leu Lys Val Ser Trp Gln Glu

325

330

335

Pro Leu Glu Lys Asn Gly Ile Ile Thr Gly Tyr Gln Ile Ser Trp Glu
340 345 350

Val Tyr Gly Arg Asn Asp Ser Arg Leu Thr His Thr Leu Asn Ser Thr
355 360 365

Met His Glu Tyr Lys Ile Gln Gly Leu Ser Ser Leu Thr Thr Tyr Thr
370 375 380

Ile Asp Val Ala Ala Val Thr Ala Val Gly Thr Gly Leu Val Thr Ser
385 390 395 400

Ser Thr Ile Ser Ser Gly Val Pro Pro Asp Leu Pro Gly Ala Pro Ser
405 410 415

Asn Leu Val Ile Ser Asn Ile Ser Pro Arg Ser Ala Thr Leu Gln Phe
420 425 430

Arg Pro Gly Tyr Asp Gly Lys Thr Ser Ile Ser Arg Trp Ile Val Glu
435 440 445

Gly Gln Met Arg Pro Glu Gly Val Gly Leu Pro Ala Glu Val Thr Gln
450 455 460

Pro Ser His Glu Ala Gly Leu Glu Pro Ala Asn Leu Gly Ser Leu Trp
465 470 475 480

Leu Leu Ser Leu Val Tyr Trp Cys Tyr Ser Gln Lys Leu Trp Glu Phe
485 490 495

Ser Cys

<210> 68

<211> 1902

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (22).. (1515)

<400> 68

gaaggaggga atgactccag g atg gcc cgg ctg gaa gtg att gaa ctg cct 51

Met Ala Arg Leu Glu Val Ile Glu Leu Pro

1

5

10

cat tca cct cag aac ctc ctg gtc agc cct aat tct tcc cac agc cac 99

His Ser Pro Gln Asn Leu Leu Val Ser Pro Asn Ser Ser His Ser His

15

20

25

gcc gtg gtg ctc tct tgg gtc cgg ccc ttt gat gga aac agt cct att 147

Ala Val Val Leu Ser Trp Val Arg Pro Phe Asp Gly Asn Ser Pro Ile

30

35

40

ctt tat tac atc gtg gag ctg tct gaa aac aac tct cca tgg aag gtg 195

Leu Tyr Tyr Ile Val Glu Leu Ser Glu Asn Asn Ser Pro Trp Lys Val

45

50

55

cat ctg tca aac gtt ggc cct gag atg aca ggc gtc acc gtg agt ggc 243

His Leu Ser Asn Val Gly Pro Glu Met Thr Gly Val Thr Val Ser Gly

60

65

70

ctg act ccg gct cgt acc tat caa ttc cgg gtg tgc gcg gtg aat gaa 291

Leu Thr Pro Ala Arg Thr Tyr Gln Phe Arg Val Cys Ala Val Asn Glu

75

80

85

90

gtg ggc agg ggc cag tac agt gcc gag aca agc agg ttg atg cta cct 339

Val Gly Arg Gly Gln Tyr Ser Ala Glu Thr Ser Arg Leu Met Leu Pro

95

100

105

gaa gaa cca ccc agt gct ccc ccg aaa aat ata gtg gcc agt ggg cgg 387

Glu Glu Pro Pro Ser Ala Pro Pro Lys Asn Ile Val Ala Ser Gly Arg

110

115

120

act aat cag tcc att atg gtc cag tgg cag cca ccc cca gaa aca gag 435

Thr Asn Gln Ser Ile Met Val Gln Trp Gln Pro Pro Pro Glu Thr Glu

125

130

135

cac aac ggg gtg ttg cgt gga tac atc ctc agg tac cgc ctg gct ggc 483

His Asn Gly Val Leu Arg Gly Tyr Ile Leu Arg Tyr Arg Leu Ala Gly

140

145

150

ctt ccc gga gag tac cag cag cgg aac atc acc agc ccg gag gtg aac 531

Leu Pro Gly Glu Tyr Gln Gln Arg Asn Ile Thr Ser Pro Glu Val Asn

155

160

165

170

tac tgc ctg gtg aca gac ctg atc atc tgg aca cag tat gag ata cag 579

Tyr Cys Leu Val Thr Asp Leu Ile Ile Trp Thr Gln Tyr Glu Ile Gln

175

180

185

gtg gcg gcg tac aac ggg gcc ggt ctg ggc gtc ttc agc agg gca gtg 627

Val Ala Ala Tyr Asn Gly Ala Gly Leu Gly Val Phe Ser Arg Ala Val

190

195

200

acc gag tac acc ttg cag gga gtg ccc acc gcg ccc ccg cag aac gtg 675

Thr Glu Tyr Thr Leu Gln Gly Val Pro Thr Ala Pro Pro Gln Asn Val

205

210

215

cag acg gaa gcc gtg aac tcc acc acc att cag ttc ctg tgg aac cct 723

Gln Thr Glu Ala Val Asn Ser Thr Thr Ile Gln Phe Leu Trp Asn Pro

220

225

230

ccg cct cag cag ttt atc aat ggc atc aac cag gga tac aag ctt ctg 771

Pro Pro Gln Gln Phe Ile Asn Gly Ile Asn Gln Gly Tyr Lys Leu Leu

235

240

245

250

gca tgg ccg gca gat gcc ccc gag gct gtc act gtg gtc act att gcc 819

Ala Trp Pro Ala Asp Ala Pro Glu Ala Val Thr Val Val Thr Ile Ala

255

260

265

cca gat ttc cac gga gtc cac cat gga cac ata acg aac ctg aag aag 867

Pro Asp Phe His Gly Val His His Gly His Ile Thr Asn Leu Lys Lys

270

275

280

ttt acc gcc tac ttc act tcc gtt ctg tgc ttc acc acc cct ggg gac 915
 Phe Thr Ala Tyr Phe Thr Ser Val Leu Cys Phe Thr Thr Pro Gly Asp

285

290

295

ggg cct ccc agc aca cct cag ctg gtc tgg act cag gaa gac aaa cca 963
 Gly Pro Pro Ser Thr Pro Gln Leu Val Trp Thr Gln Glu Asp Lys Pro

300

305

310

gga gct gig gga cat ctg agt ttc aca gag atc ttg gac aca tct ctc 1011
 Gly Ala Val Gly His Leu Ser Phe Thr Glu Ile Leu Asp Thr Ser Leu

315

320

325

330

aag gtc agc tgg cag gag ccc ctg gag aaa aat ggc atc att act ggc 1059
 Lys Val Ser Trp Gln Glu Pro Leu Glu Lys Asn Gly Ile Ile Thr Gly

335

340

345

tat cag atc tct tgg gaa gtg tac ggc agg aac gac tct cgt ctc acg 1107
 Tyr Gln Ile Ser Trp Glu Val Tyr Gly Arg Asn Asp Ser Arg Leu Thr

350

355

360

cac acc ctg aac agc acg atg cac gag tac aag atc caa ggc ctc tca 1155
 His Thr Leu Asn Ser Thr Met His Glu Tyr Lys Ile Gln Gly Leu Ser

365

370

375

tct ctc acc acc tac acc atc gac gtg gcc gct gtg act gcc gtg ggc 1203
 Ser Leu Thr Thr Tyr Thr Ile Asp Val Ala Ala Val Thr Ala Val Gly

380

385

390

act ggc ctg gtg act tca tcc acc att tct tct gga gtg ccc cca gac 1251

Thr Gly Leu Val Thr Ser Ser Thr Ile Ser Ser Gly Val Pro Pro Asp

395

400

405

410

ctt cct ggt gcc cca tcc aac ctg gtc att tcc aac atc agc cct cgc 1299

Leu Pro Gly Ala Pro Ser Asn Leu Val Ile Ser Asn Ile Ser Pro Arg

415

420

425

tcc gcc acc ctt cag ttc cgg cca ggc tat gac ggg aaa acg tcc atc 1347

Ser Ala Thr Leu Gln Phe Arg Pro Gly Tyr Asp Gly Lys Thr Ser Ile

430

435

440

tcc agg tgg att gtt gag ggg cag atg aga cct gaa ggt gtt gga tta 1395

Ser Arg Trp Ile Val Glu Gly Gln Met Arg Pro Glu Gly Val Gly Leu

445

450

455

cct gcc gag gtc aca cag cca agc cat gaa gcc gga ttg gag cct gca 1443

Pro Ala Glu Val Thr Gln Pro Ser His Glu Ala Gly Leu Glu Pro Ala

460

465

470

aac ctc gga agt ctg tgg ctg ctc agc ctg gtg tat tgg tgt tac agc 1491

Asn Leu Gly Ser Leu Trp Leu Leu Ser Leu Val Tyr Trp Cys Tyr Ser

475

480

485

490

cag aaa ctt tgg gaa ttc tct tgt tagttggta gttttactgt aattttctat 1545

Gln Lys Leu Trp Glu Phe Ser Cys

495

aaagaattca tatcatctgt taatggcgac agtttttgtt tcttcctttg aattttttat 1605

attctttctt tctctttttt gttcttctt ctttgagtat ttigtatct tactgggagg 1665

gctaaagcgt cttctatcat atcgaattgg gacaatgata gaagacaatc ttgttttgt 1725

cactctaaag aaattattgt aagattttat catcaggtat gacatttaca ccattgatgt 1785

aggcttttta aaaaatatat ccagcctgta ttgggtaag atgattcttt tctgacctg 1845

atttcctagg agttggtttt tttttttta aagcataaat aaatttaatt gcatcag 1902

<210> 69

<211> 498

<212> PRT

<213> Homo sapiens

<400> 69

Met Ala Arg Leu Glu Val Ile Glu Leu Pro His Ser Pro Gln Asn Leu

1

5

10

15

Leu Val Ser Pro Asn Ser Ser His Ser His Ala Val Val Leu Ser Trp

20

25

30

Val Arg Pro Phe Asp Gly Asn Ser Pro Ile Leu Tyr Tyr Ile Val Glu

35

40

45

Leu Ser Glu Asn Asn Ser Pro Trp Lys Val His Leu Ser Asn Val Gly

50

55

60

Pro Glu Met Thr Gly Val Thr Val Ser Gly Leu Thr Pro Ala Arg Thr
65 70 75 80

Tyr Gln Phe Arg Val Cys Ala Val Asn Glu Val Gly Arg Gly Gln Tyr
85 90 95

Ser Ala Glu Thr Ser Arg Leu Met Leu Pro Glu Glu Pro Pro Ser Ala
100 105 110

Pro Pro Lys Asn Ile Val Ala Ser Gly Arg Thr Asn Gln Ser Ile Met
115 120 125

Val Gln Trp Gln Pro Pro Pro Glu Thr Glu His Asn Gly Val Leu Arg
130 135 140

Gly Tyr Ile Leu Arg Tyr Arg Leu Ala Gly Leu Pro Gly Glu Tyr Gln
145 150 155 160

Gln Arg Asn Ile Thr Ser Pro Glu Val Asn Tyr Cys Leu Val Thr Asp
165 170 175

Leu Ile Ile Trp Thr Gln Tyr Glu Ile Gln Val Ala Ala Tyr Asn Gly
180 185 190

Ala Gly Leu Gly Val Phe Ser Arg Ala Val Thr Glu Tyr Thr Leu Gln
195 200 205

Gly Val Pro Thr Ala Pro Pro Gln Asn Val Gln Thr Glu Ala Val Asn
210 215 220

Ser Thr Thr Ile Gln Phe Leu Trp Asn Pro Pro Pro Gln Gln Phe Ile
225 230 235 240

Asn Gly Ile Asn Gln Gly Tyr Lys Leu Leu Ala Trp Pro Ala Asp Ala
245 250 255

Pro Glu Ala Val Thr Val Val Thr Ile Ala Pro Asp Phe His Gly Val
260 265 270

His His Gly His Ile Thr Asn Leu Lys Lys Phe Thr Ala Tyr Phe Thr
275 280 285

Ser Val Leu Cys Phe Thr Thr Pro Gly Asp Gly Pro Pro Ser Thr Pro
290 295 300

Gln Leu Val Trp Thr Gln Glu Asp Lys Pro Gly Ala Val Gly His Leu
305 310 315 320

Ser Phe Thr Glu Ile Leu Asp Thr Ser Leu Lys Val Ser Trp Gln Glu
325 330 335

Pro Leu Glu Lys Asn Gly Ile Ile Thr Gly Tyr Gln Ile Ser Trp Glu
340 345 350

Val Tyr Gly Arg Asn Asp Ser Arg Leu Thr His Thr Leu Asn Ser Thr
355 360 365

Thr His Glu Tyr Lys Ile Gln Gly Leu Ser Ser Leu Thr Thr Tyr Thr

370

375

380

Ile Asp Val Ala Ala Val Thr Ala Val Gly Thr Gly Leu Val Thr Ser

385

390

395

400

Ser Thr Ile Ser Ser Gly Val Pro Pro Asp Leu Pro Gly Ala Pro Ser

405

410

415

Asn Leu Val Ile Ser Asn Ile Ser Pro Arg Ser Ala Thr Leu Gln Phe

420

425

430

Arg Pro Gly Tyr Asp Gly Lys Thr Ser Ile Ser Arg Trp Ile Val Glu

435

440

445

Gly Gln Met Arg His Gln Gly Val Gly Leu Pro Ala Glu Val Thr Gln

450

455

460

Pro Ser His Glu Ala Gly Leu Glu Pro Ala Asn Leu Gly Ser Leu Trp

465

470

475

480

Leu Leu Ser Leu Val Tyr Trp Cys Tyr Ser Gln Lys Leu Trp Glu Phe

485

490

495

Ser Cys

<210> 70

<211> 1902

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (22).. (1515)

<400> 70

gaaggaggga atgactccag g atg gcc cgg ctg gaa gtg att gaa ctg cct 51

Met Ala Arg Leu Glu Val Ile Glu Leu Pro

1 5 10

cat tca cct cag aac ctc ctg gtc agc cct aat tct tcc cac agc cac 99

His Ser Pro Gln Asn Leu Leu Val Ser Pro Asn Ser Ser His Ser His

15 20 25

gcc gtg gtg ctc tct tgg gtc cgg ccc ttt gat gga aac agt cct att 147

Ala Val Val Leu Ser Trp Val Arg Pro Phe Asp Gly Asn Ser Pro Ile

30 35 40

ctt tat tac atc gtg gag ctg tct gaa aac aac tct cca tgg aag gtg 195

Leu Tyr Tyr Ile Val Glu Leu Ser Glu Asn Asn Ser Pro Trp Lys Val

45 50 55

cat ctg tca aac gtt ggc cct gag atg aca ggc gtc acc gtg agt ggc 243

His Leu Ser Asn Val Gly Pro Glu Met Thr Gly Val Thr Val Ser Gly

60 65 70

ctg act ccg gct cgt acc tat caa ttc cgg gtg tgc gcg gtg aat gaa 291

Leu Thr Pro Ala Arg Thr Tyr Gln Phe Arg Val Cys Ala Val Asn Glu
 75 80 85 90

gtg ggc agg ggc cag tac agt gcc gag aca agc agg ttg atg cta cct 339
 Val Gly Arg Gly Gln Tyr Ser Ala Glu Thr Ser Arg Leu Met Leu Pro
 95 100 105

gaa gaa cca ccc agt gct ccc ccg aaa aat ata gtg gcc agt ggg cgg 387
 Glu Glu Pro Pro Ser Ala Pro Pro Lys Asn Ile Val Ala Ser Gly Arg
 110 115 120

act aat cag tcc att atg gtc cag tgg cag cca ccc cca gaa aca gag 435
 Thr Asn Gln Ser Ile Met Val Gln Trp Gln Pro Pro Pro Glu Thr Glu
 125 130 135

cac aac ggg gtg ttg cgt gga tac atc ctc agg tac cgc ctg gct ggc 483
 His Asn Gly Val Leu Arg Gly Tyr Ile Leu Arg Tyr Arg Leu Ala Gly
 140 145 150

ctt ccc gga gag tac cag cag cgg aac atc acc agc ccg gag gtg aac 531
 Leu Pro Gly Glu Tyr Gln Gln Arg Asn Ile Thr Ser Pro Glu Val Asn
 155 160 165 170

tac tgc ctg gtg aca gac ctg atc atc tgg aca cag tat gag ata cag 579
 Tyr Cys Leu Val Thr Asp Leu Ile Ile Trp Thr Gln Tyr Glu Ile Gln
 175 180 185

gtg gcg gcg tac aac ggg gcc ggt ctg ggc gtc ttc agc agg gca gtg 627
 Val Ala Ala Tyr Asn Gly Ala Gly Leu Gly Val Phe Ser Arg Ala Val

190

195

200

acc gag tac acc ttg cag gga gtg ccc acc gcg ccc ccg cag aac gtg 675

Thr Glu Tyr Thr Leu Gln Gly Val Pro Thr Ala Pro Pro Gln Asn Val

205

210

215

cag acg gaa gcc gtg aac tcc acc acc att cag ttc ctg tgg aac cct 723

Gln Thr Glu Ala Val Asn Ser Thr Thr Ile Gln Phe Leu Trp Asn Pro

220

225

230

ccg cct cag cag ttt atc aat ggc atc aac cag gga tac aag ctt ctg 771

Pro Pro Gln Gln Phe Ile Asn Gly Ile Asn Gln Gly Tyr Lys Leu Leu

235

240

245

250

gca tgg ccg gca gat gcc ccc gag gct gtc act gtg gtc act att gcc 819

Ala Trp Pro Ala Asp Ala Pro Glu Ala Val Thr Val Val Thr Ile Ala

255

260

265

cca gat ttc cac gga gtc cac cat gga cac ata acg aac ctg aag aag 867

Pro Asp Phe His Gly Val His His Gly His Ile Thr Asn Leu Lys Lys

270

275

280

ttt acc gcc tac ttc act tcc gtt ctg tgc ttc acc acc cct ggg gac 915

Phe Thr Ala Tyr Phe Thr Ser Val Leu Cys Phe Thr Thr Pro Gly Asp

285

290

295

ggg cct ccc agc aca cct cag ctg gtc tgg act cag gaa gac aaa cca 963

Gly Pro Pro Ser Thr Pro Gln Leu Val Trp Thr Gln Glu Asp Lys Pro

300

305

310

gga gct gtg gga cat ctg agt ttc aca gag atc ttg gac aca tct ctc 1011

Gly Ala Val Gly His Leu Ser Phe Thr Glu Ile Leu Asp Thr Ser Leu

315

320

325

330

aag gtc agc tgg cag gag ccc ctg gag aaa aat ggc atc att act ggc 1059

Lys Val Ser Trp Gln Glu Pro Leu Glu Lys Asn Gly Ile Ile Thr Gly

335

340

345

tat cag atc tct tgg gaa gtg tac ggc agg aac gac tct cgt ctc acg 1107

Tyr Gln Ile Ser Trp Glu Val Tyr Gly Arg Asn Asp Ser Arg Leu Thr

350

355

360

cac acc ctg aac agc acg acg cac gag tac aag atc caa ggc ctc tca 1155

His Thr Leu Asn Ser Thr Thr His Glu Tyr Lys Ile Gln Gly Leu Ser

365

370

375

tct ctc acc acc tac acc atc gac gtg gcc gct gtg act gcc gtg ggc 1203

Ser Leu Thr Thr Tyr Thr Ile Asp Val Ala Ala Val Thr Ala Val Gly

380

385

390

act ggc ctg gtg act tca tcc acc att tct tct gga gtg ccc cca gac 1251

Thr Gly Leu Val Thr Ser Ser Thr Ile Ser Ser Gly Val Pro Pro Asp

395

400

405

410

ctt cct ggt gcc cca tcc aac ctg gtc att tcc aac atc agc cct cgc 1299

Leu Pro Gly Ala Pro Ser Asn Leu Val Ile Ser Asn Ile Ser Pro Arg

415

420

425

tcc gcc acc ctt cag ttc cgg cca ggc tat gac ggg aaa acg tcc atc 1347
Ser Ala Thr Leu Gln Phe Arg Pro Gly Tyr Asp Gly Lys Thr Ser Ile

430

435

440

tcc agg tgg att gtt gag ggg cag atg aga cat caa ggt gtl gga tta 1395
Ser Arg Trp Ile Val Glu Gly Gln Met Arg His Gln Gly Val Gly Leu

445

450

455

cct gcc gag gtc aca cag cca agc cat gaa gcc gga ttg gag cct gca 1443
Pro Ala Glu Val Thr Gln Pro Ser His Glu Ala Gly Leu Glu Pro Ala

460

465

470

aac ctc gga agt ctg tgg ctg ctc agc ctg gtg tat tgg tgt tac agc 1491
Asn Leu Gly Ser Leu Trp Leu Leu Ser Leu Val Tyr Trp Cys Tyr Ser

475

480

485

490

cag aaa ctt tgg gaa ttc tct tgt tagttggta gttttactgt aattttctat 1545
Gln Lys Leu Trp Glu Phe Ser Cys

495

aaagaattca tatcatctgt taatggcgac agtttttgtt tcttcctttg aattttttat 1605

attctttctt tctctttttt gtttcttctt ctttgagtat ttgtaatct tactgggagg 1665

gctaaagcgt cttctatcat atcgaattgg gacaatgata gaagacaatc ttgtttttgt 1725

cactctaaag aaattattgt aagattttat catcaggat gacatttaca ccattgatgt 1785

aggcttttta aaaaatatat ccagcctgta ttgggttaag atgattcttt tctgacctg 1845

atttcctagg agttggtttt ttttttttta aagcataaaat aaattttaatt gcatcag 1902

<210> 71

<211> 245

<212> PRT

<213> Homo sapiens

<400> 71

Met Pro Val Gln Leu Ser Glu His Pro Glu Trp Asn Glu Ser Met His

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Ser Leu Arg Ile Ser Val Gly Gly Leu Pro Val Leu Ala Ser Met Thr

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25

30

Lys Ala Ala Asp Pro Arg Phe Arg Pro Arg Trp Lys Val Ile Leu Thr

35

40

45

Phe Phe Val Gly Ala Ala Ile Leu Trp Leu Leu Cys Ser His Arg Pro

50

55

60

Ala Pro Gly Arg Pro Pro Thr His Asn Ala His Asn Trp Arg Leu Gly

65

70

75

80

Gln Ala Pro Ala Asn Trp Tyr Asn Asp Thr Tyr Pro Leu Ser Pro Pro

85

90

95

Gln Arg Thr Pro Ala Gly Ile Arg Tyr Arg Ile Ala Val Ile Ala Asp

100

105

110

Leu Asp Thr Glu Ser Arg Ala Gln Glu Glu Asn Thr Trp Phe Ser Tyr

115

120

125

Leu Lys Lys Gly Tyr Leu Thr Leu Ser Asp Ser Gly Asp Lys Val Ala

130

135

140

Val Glu Trp Asp Lys Asp His Gly Val Leu Glu Ser His Leu Ala Glu

145

150

155

160

Lys Gly Arg Gly Met Glu Leu Ser Asp Leu Ile Val Phe Asn Gly Lys

165

170

175

Leu Tyr Ser Val Asp Asp Arg Thr Gly Val Val Tyr Gln Ile Glu Gly

180

185

190

Ser Lys Ala Val Pro Trp Val Ile Leu Ser Asp Gly Asp Gly Thr Val

195

200

205

Glu Lys Gly Phe Lys Ala Glu Trp Leu Ala Val Arg Glu Ile Val Arg

210

215

220

Lys Arg Trp Arg Leu Val Lys Gln Val Ser His Val Gly Val Leu Gly

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Gln Trp Ile Gln Arg

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<210> 72

<211> 1551

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (127).. (861)

<400> 72

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ccaagccccg ccgctcgccg gcaccggagc cagccccgca gcgggtcccg cctgtctgtc 120

acgctg atg ccc gtg cag ctg tct gag cac ccg gaa tgg aat gag tct 168

Met Pro Val Gln Leu Ser Glu His Pro Glu Trp Asn Glu Ser

1

5

10

atg cac tcc ctc cgg atc agt gtg ggg ggc ctt cct gtg ctg gcg tcc 216

Met His Ser Leu Arg Ile Ser Val Gly Gly Leu Pro Val Leu Ala Ser

15

20

25

30

atg acc aag gcc gcg gac ccc cgc ttc cgc ccc cgc tgg aag gtg atc 264

Met Thr Lys Ala Ala Asp Pro Arg Phe Arg Pro Arg Trp Lys Val Ile

35

40

45

ctg acg ttc ttt gtg ggt gct gcc atc ctc tgg ctg ctc tgc tcc cac 312

Leu Thr Phe Phe Val Gly Ala Ala Ile Leu Trp Leu Leu Cys Ser His

50

55

60

cgc ccg gcc ccc ggc agg ccc ccc acc cac aat gca cac aac tgg agg 360

Arg Pro Ala Pro Gly Arg Pro Pro Thr His Asn Ala His Asn Trp Arg

65

70

75

ctc ggc cag gcg ccc gcc aac tgg tac aat gac acc tac ccc ctg tct 408

Leu Gly Gln Ala Pro Ala Asn Trp Tyr Asn Asp Thr Tyr Pro Leu Ser

80

85

90

ccc cca caa agg aca ccg gct ggg att cgg tat cga atc gca gtt atc 456

Pro Pro Gln Arg Thr Pro Ala Gly Ile Arg Tyr Arg Ile Ala Val Ile

95

100

105

110

gca gac ctg gac aca gag tca agg gcc caa gag gaa aac acc tgg ttc 504

Ala Asp Leu Asp Thr Glu Ser Arg Ala Gln Glu Glu Asn Thr Trp Phe

115

120

125

agt tac ctg aaa aag ggc tac ctg acc ctg tca gac agt ggg gac aag 552

Ser Tyr Leu Lys Lys Gly Tyr Leu Thr Leu Ser Asp Ser Gly Asp Lys

130

135

140

gtg gcc gtg gaa tgg gac aaa gac cat ggg gtc ctg gag tcc cac ctg 600

Val Ala Val Glu Trp Asp Lys Asp His Gly Val Leu Glu Ser His Leu

145

150

155

gcg gag aag ggg aga ggc atg gag cta tcc gac ctg att gtt ttc aat 648

Ala Glu Lys Gly Arg Gly Met Glu Leu Ser Asp Leu Ile Val Phe Asn

160

165

170

ggg aaa ctc tac tcc gtg gat gac cgg acg ggg gtc gtc tac cag atc 696
Gly Lys Leu Tyr Ser Val Asp Asp Arg Thr Gly Val Val Tyr Gln Ile
175 180 185 190

gaa ggc agc aaa gcc gtg ccc tgg gtg att ctg tcc gac ggc gac ggc 744
Glu Gly Ser Lys Ala Val Pro Trp Val Ile Leu Ser Asp Gly Asp Gly
195 200 205

acc gtg gag aaa ggc ttc aag gcc gaa tgg ctg gca gtg cgg gag att 792
Thr Val Glu Lys Gly Phe Lys Ala Glu Trp Leu Ala Val Arg Glu Ile
210 215 220

gta agg aag cgg tgg cgg ctg gtg aag caa gtc tca cat gtc ggc gtt 840
Val Arg Lys Arg Trp Arg Leu Val Lys Gln Val Ser His Val Gly Val
225 230 235

ctt ggc caa tgg ata caa aga taaagaaaat gttgcctttt tctaggaact 891
Leu Gly Gln Trp Ile Gln Arg
240 245

gtcagaaatc ctcatgcctt tcaagacttc tgtgaatgac ttgaattttt tattccctgc 951

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<210> 73

<211> 352

<212> PRT

<213> Homo sapiens

<400> 73

Met Glu Ser Gly Gly Arg Pro Ser Leu Cys Gln Phe Ile Leu Leu Gly

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10

15

Thr Thr Ser Val Val Thr Ala Ala Leu Tyr Ser Val Tyr Arg Gln Lys

20

25

30

Ala Arg Val Ser Gln Glu Leu Lys Gly Ala Lys Lys Val His Leu Gly

35

40

45

Glu Asp Leu Lys Ser Ile Leu Ser Glu Ala Pro Gly Lys Cys Val Pro
50 55 60

Tyr Ala Val Ile Glu Gly Ala Val Arg Ser Val Lys Glu Thr Leu Asn
65 70 75 80

Ser Gln Phe Val Glu Asn Cys Lys Gly Val Ile Gln Arg Leu Thr Leu
85 90 95

Gln Glu His Lys Met Val Trp Asn Arg Thr Thr His Leu Trp Asn Asp
100 105 110

Cys Ser Lys Ile Ile His Gln Arg Thr Asn Thr Val Pro Phe Asp Leu
115 120 125

Val Pro His Glu Asp Gly Val Asp Val Ala Val Arg Val Leu Lys Pro
130 135 140

Leu Asp Ser Val Asp Leu Gly Leu Glu Thr Val Tyr Glu Lys Phe His
145 150 155 160

Pro Ser Ile Gln Ser Phe Thr Asp Val Ile Gly His Tyr Ile Ser Gly
165 170 175

Glu Arg Pro Lys Gly Ile Gln Glu Thr Glu Glu Met Leu Lys Val Gly
180 185 190

Ala Thr Leu Thr Gly Val Gly Glu Leu Val Leu Asp Asn Asn Ser Val

195	200	205
Arg Leu Gln Pro Pro Lys Gln Gly Met Gln Tyr Tyr Leu Ser Ser Gln		
210	215	220
Asp Phe Asp Ser Leu Leu Gln Arg Gln Glu Ser Ser Val Arg Leu Trp		
225	230	235 240
Lys Val Leu Ala Leu Val Phe Gly Phe Ala Thr Cys Ala Thr Leu Phe		
245	250	255
Phe Ile Leu Arg Lys Gln Tyr Leu Gln Arg Gln Glu Arg Leu Arg Leu		
260	265	270
Lys Gln Met Gln Glu Glu Phe Gln Glu His Glu Ala Gln Leu Leu Ser		
275	280	285
Arg Ala Lys Pro Glu Asp Arg Glu Ser Leu Lys Ser Ala Cys Val Val		
290	295	300
Cys Leu Ser Ser Phe Lys Ser Cys Val Phe Leu Glu Cys Gly His Val		
305	310	315 320
Cys Ser Cys Thr Glu Cys Tyr Arg Ala Leu Pro Glu Pro Lys Lys Cys		
325	330	335
Pro Ile Cys Arg Gln Ala Ile Thr Arg Val Ile Pro Pro Tyr Asn Ser		
340	345	350

<210> 74

<211> 2401

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (103).. (1158)

<400> 74

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tataccttggc gccacagtcg gccaccgggg ctcgccgccg tc atg gag agc gga 114

Met Glu Ser Gly

1

ggg cgg ccc tcg ctg tgc cag ttc atc ctc ctg ggc acc acc tct gtg 162

Gly Arg Pro Ser Leu Cys Gln Phe Ile Leu Leu Gly Thr Thr Ser Val

5

10

15

20

gtc acc gcc gcc ctg tac tcc gtg tac cgg cag aag gcc cgg gtc tcc 210

Val Thr Ala Ala Leu Tyr Ser Val Tyr Arg Gln Lys Ala Arg Val Ser

25

30

35

caa gag ctc aag gga gct aaa aaa gtt cat ttg ggt gaa gat tta aag 258

Gln Glu Leu Lys Gly Ala Lys Lys Val His Leu Gly Glu Asp Leu Lys

40

45

50

agt att ctt tca gaa gct cca gga aaa tgc gtg cct tat gct gtt ata 306
 Ser Ile Leu Ser Glu Ala Pro Gly Lys Cys Val Pro Tyr Ala Val Ile
 55 60 65

gaa gga gct gtg cgg tct gtt aaa gaa acg ctt aac agc cag ttt gtg 354
 Glu Gly Ala Val Arg Ser Val Lys Glu Thr Leu Asn Ser Gln Phe Val
 70 75 80

gaa aac tgc aag ggg gta att cag cgg ctg aca ctt cag gag cac aag 402
 Glu Asn Cys Lys Gly Val Ile Gln Arg Leu Thr Leu Gln Glu His Lys
 85 90 95 100

atg gtg tgg aat cga acc acc cac ctt tgg aat gat tgc tca aag atc 450
 Met Val Trp Asn Arg Thr Thr His Leu Trp Asn Asp Cys Ser Lys Ile
 105 110 115

att cat cag agg acc aac aca gtg ccc ttt gac ctg gtg ccc cac gag 498
 Ile His Gln Arg Thr Asn Thr Val Pro Phe Asp Leu Val Pro His Glu
 120 125 130

gat ggc gtg gat gtg gct gtg cga gtg ctg aag ccc ctg gac tca gtg 546
 Asp Gly Val Asp Val Ala Val Arg Val Leu Lys Pro Leu Asp Ser Val
 135 140 145

gat ctg ggt cta gag act gtg tat gag aag ttc cac ccc tgc att cag 594
 Asp Leu Gly Leu Glu Thr Val Tyr Glu Lys Phe His Pro Ser Ile Gln
 150 155 160

tcc ttc acc gat gtc atc ggc cac tac atc agc ggt gag cgg ccc aaa 642

Ser Phe Thr Asp Val Ile Gly His Tyr Ile Ser Gly Glu Arg Pro Lys
 165 170 175 180

ggc atc caa gag acc gag gag atg ctg aag gtg ggg gcc acc ctc aca 690
 Gly Ile Gln Glu Thr Glu Glu Met Leu Lys Val Gly Ala Thr Leu Thr
 185 190 195

ggg gtt ggc gaa ctg gtc ctg gac aac aac tct gtc cgc ctg cag ccg 738
 Gly Val Gly Glu Leu Val Leu Asp Asn Asn Ser Val Arg Leu Gln Pro
 200 205 210

ccc aaa caa ggc atg cag tac tat cta agc agc cag gac ttc gac agc 786
 Pro Lys Gln Gly Met Gln Tyr Tyr Leu Ser Ser Gln Asp Phe Asp Ser
 215 220 225

ctg ctg cag agg cag gag tcg agc gtc agg ctc tgg aag gtg ctg gcg 834
 Leu Leu Gln Arg Gln Glu Ser Ser Val Arg Leu Trp Lys Val Leu Ala
 230 235 240

ctg gtt ttt ggc ttt gcc aca tgt gcc acc ctc ttc ttc att ctc cgg 882
 Leu Val Phe Gly Phe Ala Thr Cys Ala Thr Leu Phe Phe Ile Leu Arg
 245 250 255 260

aag cag tat ctg cag cgg cag gag cgc ctg cgc ctc aag cag atg cag 930
 Lys Gln Tyr Leu Gln Arg Gln Glu Arg Leu Arg Leu Lys Gln Met Gln
 265 270 275

gag gag ttc cag gag cat gag gcc cag ctg ctg agc cga gcc aag cct 978
 Glu Glu Phe Gln Glu His Glu Ala Gln Leu Leu Ser Arg Ala Lys Pro

280

285

290

gag gac agg gag agt ctg aag agc gcc tgt gta gtg tgt ctg agc agc 1026

Glu Asp Arg Glu Ser Leu Lys Ser Ala Cys Val Val Cys Leu Ser Ser

295

300

305

ttc aag tcc tgc gtc ttt ctg gag tgt ggg cac gtt tgt tcc tgc acc 1074

Phe Lys Ser Cys Val Phe Leu Glu Cys Gly His Val Cys Ser Cys Thr

310

315

320

gag tgc tac cgc gcc ttg cca gag ccc aag aag tgc cct atc tgc aga 1122

Glu Cys Tyr Arg Ala Leu Pro Glu Pro Lys Lys Cys Pro Ile Cys Arg

325

330

335

340

cag gcg atc acc cgg gtg ata ccc ccg tac aac agc taatagtttg 1168

Gln Ala Ile Thr Arg Val Ile Pro Pro Tyr Asn Ser

345

350

gaagccgcac agcttgacct ggaagcacc ctcgccccctt ttcagggaatt tttatctcga 1228

ggccittgga ggagcagtgg tgggggtagc tgtcacctcc aggtatgatt gagggaggaa 1288

tcgggtagaa actctccaga cccatgcctc caatggcagg atgtgcctt tcccacctga 1348

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gtgtgaacag cagaaattaa acatgttgca acc

2401

<210> 75

<211> 352

<212> PRT

<213> Homo sapiens

<400> 75

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Thr Thr Ser Val Val Thr Ala Ala Leu Tyr Ser Val Tyr Arg Gln Lys

20 25 30

Ala Arg Val Ser Gln Glu Leu Lys Gly Ala Lys Lys Val His Leu Gly

35 40 45

Glu Asp Leu Lys Ser Ile Leu Ser Glu Ala Pro Gly Lys Cys Val Pro

50 55 60

Tyr Ala Val Ile Glu Gly Ala Val Arg Ser Val Lys Glu Thr Leu Asn

65 70 75 80

Ser Gln Phe Val Glu Asn Cys Lys Gly Val Ile Gln Arg Leu Thr Leu

85 90 95

Gln Glu His Lys Met Val Trp Asn Arg Thr Thr His Leu Trp Asn Asp

100 105 110

Cys Ser Lys Ile Ile His Gln Arg Thr Asn Thr Val Pro Phe Asp Leu

115

120

125

Val Pro His Glu Asp Gly Val Asp Val Ala Val Arg Val Leu Lys Pro

130

135

140

Leu Asp Ser Val Asp Leu Gly Leu Glu Thr Val Tyr Glu Lys Phe His

145

150

155

160

Pro Ser Ile Gln Ser Phe Thr Asp Val Ile Gly His Tyr Ile Ser Gly

165

170

175

Glu Arg Pro Lys Gly Ile Gln Glu Thr Glu Glu Met Leu Lys Val Gly

180

185

190

Ala Thr Leu Thr Gly Val Gly Glu Leu Val Leu Asp Asn Asn Ser Val

195

200

205

Arg Leu Gln Pro Pro Lys Gln Gly Met Gln Tyr Tyr Leu Ser Ser Gln

210

215

220

Asp Phe Asp Ser Leu Leu Gln Arg Gln Glu Ser Ser Val Arg Leu Trp

225

230

235

240

Lys Val Leu Ala Leu Val Phe Gly Phe Ala Thr Cys Ala Thr Leu Phe

245

250

255

Phe Ile Leu Arg Lys Gln Tyr Leu Gln Arg Gln Glu Arg Leu Arg Leu

260

265

270

Lys Gln Met Gln Glu Glu Phe Gln Glu His Glu Ala Gln Leu Leu Ser

275

280

285

Arg Ala Lys Pro Glu Asp Arg Glu Ser Leu Lys Ser Ala Cys Val Val

290

295

300

Cys Leu Ser Ser Phe Lys Ser Cys Val Phe Leu Glu Cys Gly His Val

305

310

315

320

Cys Ser Cys Thr Glu Cys Tyr Arg Ala Leu Pro Glu Pro Lys Lys Cys

325

330

335

Pro Ile Cys Arg Gln Ala Ile Thr Arg Val Ile Pro Leu Tyr Asn Ser

340

345

350

<210> 76

<211> 2401

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (103).. (1158)

<400> 76

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tatccttggc gccacagtcg gccaccgggg ctcgccgccg tc atg gag agc gga 114

Met Glu Ser Gly

1

ggg cgg ccc tcg ctg tgc cag ttc atc ctc ctg ggc acc acc tct gtg 162

Gly Arg Pro Ser Leu Cys Gln Phe Ile Leu Leu Gly Thr Thr Ser Val

5

10

15

20

gtc acc gcc gcc ctg tac tcc gtg tac cgg cag aag gcc cgg gtc tcc 210

Val Thr Ala Ala Leu Tyr Ser Val Tyr Arg Gln Lys Ala Arg Val Ser

25

30

35

caa gag ctc aag gga gct aaa aaa gtt cat ttg ggt gaa gat tta aag 258

Gln Glu Leu Lys Gly Ala Lys Lys Val His Leu Gly Glu Asp Leu Lys

40

45

50

agt att ctt tca gaa gct cca gga aaa tgc gtg cct tat gct gtt ata 306

Ser Ile Leu Ser Glu Ala Pro Gly Lys Cys Val Pro Tyr Ala Val Ile

55

60

65

gaa gga gct gtg cgg tct gtt aaa gaa acg ctt aac agc cag ttt gtg 354

Glu Gly Ala Val Arg Ser Val Lys Glu Thr Leu Asn Ser Gln Phe Val

70

75

80

gaa aac tgc aag ggg gta att cag cgg ctg aca ctt cag gag cac aag 402

Glu Asn Cys Lys Gly Val Ile Gln Arg Leu Thr Leu Gln Glu His Lys

85

90

95

100

atg gtg tgg aat cga acc acc cac ctt tgg aat gat tgc tca aag atc 450
Met Val Trp Asn Arg Thr Thr His Leu Trp Asn Asp Cys Ser Lys Ile

105

110

115

att cat cag agg acc aac aca gtg ccc ttt gac ctg gtg ccc cac gag 498
Ile His Gln Arg Thr Asn Thr Val Pro Phe Asp Leu Val Pro His Glu

120

125

130

gat ggc gtg gat gtg gct gtg cga gtg ctg aag ccc ctg gac tca gtg 546
Asp Gly Val Asp Val Ala Val Arg Val Leu Lys Pro Leu Asp Ser Val

135

140

145

gat ctg ggt cta gag act gtg tat gag aag ttc cac ccc tcg att cag 594
Asp Leu Gly Leu Glu Thr Val Tyr Glu Lys Phe His Pro Ser Ile Gln

150

155

160

tcc ttc acc gat gtc atc ggc cac tac atc agc ggt gag cgg ccc aaa 642
Ser Phe Thr Asp Val Ile Gly His Tyr Ile Ser Gly Glu Arg Pro Lys
165 170 175 180

ggc atc caa gag acc gag gag atg ctg aag gtg ggg gcc acc ctc aca 690
Gly Ile Gln Glu Thr Glu Glu Met Leu Lys Val Gly Ala Thr Leu Thr

185

190

195

ggg gtt ggc gaa ctg gtc ctg gac aac aac tct gtc cgc ctg cag ccg 738
Gly Val Gly Glu Leu Val Leu Asp Asn Asn Ser Val Arg Leu Gln Pro

200

205

210

ccc aaa caa ggc atg cag tac tat cta agc agc cag gac ttc gac agc 786

Pro Lys Gln Gly Met Gln Tyr Tyr Leu Ser Ser Gln Asp Phe Asp Ser
 215 220 225

ctg ctg cag agg cag gag tcg agc gtc agg ctc tgg aag gtg ctg gcg 834
 Leu Leu Gln Arg Gln Glu Ser Ser Val Arg Leu Trp Lys Val Leu Ala
 230 235 240

ctg gtt ttt ggc ttt gcc aca tgt gcc acc ctc ttc ttc att ctc cgg 882
 Leu Val Phe Gly Phe Ala Thr Cys Ala Thr Leu Phe Phe Ile Leu Arg
 245 250 255 260

aag cag tat ctg cag cgg cag gag cgc ctg cgc ctc aag cag atg cag 930
 Lys Gln Tyr Leu Gln Arg Gln Glu Arg Leu Arg Leu Lys Gln Met Gln
 265 270 275

gag gag ttc cag gag cat gag gcc cag ctg ctg agc cga gcc aag cct 978
 Glu Glu Phe Gln Glu His Glu Ala Gln Leu Leu Ser Arg Ala Lys Pro
 280 285 290

gag gac agg gag agt ctg aag agc gcc tgt gta gtg tgt ctg agc agc 1026
 Glu Asp Arg Glu Ser Leu Lys Ser Ala Cys Val Val Cys Leu Ser Ser
 295 300 305

ttc aag tcc tgc gtc ttt ctg gag tgt ggg cac gtt tgt tcc tgc acc 1074
 Phe Lys Ser Cys Val Phe Leu Glu Cys Gly His Val Cys Ser Cys Thr
 310 315 320

gag tgc tac cgc gcc ttg cca gag ccc aag aag tgc cct atc tgc aga 1122
 Glu Cys Tyr Arg Ala Leu Pro Glu Pro Lys Lys Cys Pro Ile Cys Arg

325

330

335

340

cag gcg atc acc cgg gtg ata ccc ctg tac aac agc taatagttag 1168

Gln Ala Ile Thr Arg Val Ile Pro Leu Tyr Asn Ser

345

350

gaagccgcac agcctgacct ggaagcacc ctgccccctt ttcagggtt tttatctcga 1228

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<210> 77

<211> 697

<212> PRT

<213> Homo sapiens

<400> 77

Met Cys Lys Ser Leu Arg Tyr Cys Phe Ser His Cys Leu Tyr Leu Ala

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Met Thr Arg Leu Glu Glu Val Asn Arg Glu Val Asn Met His Ser Ser

20

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30

Val Arg Tyr Leu Gly Tyr Leu Ala Arg Ile Asn Leu Leu Val Ala Ile

35

40

45

Cys Leu Gly Leu Tyr Val Arg Trp Glu Lys Thr Ala Asn Ser Leu Ile

50

55

60

Leu Val Ile Phe Ile Leu Gly Leu Phe Val Leu Gly Ile Ala Ser Ile

65

70

75

80

Leu Tyr Tyr Tyr Phe Ser Met Glu Ala Ala Ser Leu Ser Leu Ser Asn

85

90

95

Leu Trp Phe Gly Phe Leu Leu Gly Leu Leu Cys Phe Leu Asp Asn Ser

100

105

110

Ser Phe Lys Asn Asp Val Lys Glu Glu Ser Thr Lys Tyr Leu Leu Leu

115

120

125

Thr Ser Ile Val Leu Arg Ile Leu Cys Ser Leu Val Glu Arg Ile Ser

130

135

140

Gly Tyr Val Arg His Arg Pro Thr Leu Leu Thr Thr Val Glu Phe Leu

145

150

155

160

Glu Leu Val Gly Phe Ala Ile Ala Ser Thr Thr Met Leu Val Glu Lys

165

170

175

Ser Leu Ser Val Ile Leu Leu Val Val Ala Leu Ala Met Leu Ile Ile
180 185 190

Asp Leu Arg Met Lys Ser Phe Leu Ala Ile Pro Asn Leu Val Ile Phe
195 200 205

Ala Val Leu Leu Phe Phe Ser Ser Leu Glu Thr Pro Lys Asn Pro Ile
210 215 220

Ala Phe Ala Cys Phe Phe Ile Cys Leu Ile Thr Asp Pro Phe Leu Asp
225 230 235 240

Ile Tyr Phe Ser Gly Leu Ser Val Thr Glu Arg Trp Lys Pro Phe Leu
245 250 255

Tyr Arg Gly Arg Ile Cys Arg Arg Leu Ser Val Val Phe Ala Gly Met
260 265 270

Ile Glu Leu Thr Phe Phe Ile Leu Ser Ala Phe Lys Leu Arg Asp Thr
275 280 285

His Leu Trp Tyr Phe Val Ile Pro Gly Phe Ser Ile Phe Gly Ile Phe
290 295 300

Trp Met Ile Cys His Ile Ile Phe Leu Leu Thr Leu Trp Gly Phe His
305 310 315 320

Thr Lys Leu Asn Asp Cys His Lys Val Tyr Phe Thr His Arg Thr Asp

325

330

335

Tyr Asn Ser Leu Asp Arg Ile Met Ala Ser Lys Gly Met Arg His Phe

340

345

350

Cys Leu Ile Ser Glu Gln Leu Val Phe Phe Ser Leu Leu Ala Thr Ala

355

360

365

Ile Leu Gly Ala Val Ser Trp Gln Pro Thr Asn Gly Ile Phe Leu Ser

370

375

380

Met Phe Leu Ile Val Leu Pro Leu Glu Ser Met Ala His Gly Leu Phe

385

390

395

400

His Glu Leu Gly Asn Cys Leu Gly Gly Thr Ser Val Gly Tyr Ala Ile

405

410

415

Val Ile Pro Thr Asn Phe Cys Ser Pro Asp Gly Gln Pro Thr Leu Leu

420

425

430

Pro Pro Glu His Val Gln Glu Leu Asn Leu Arg Ser Thr Gly Met Leu

435

440

445

Asn Ala Ile Gln Arg Phe Phe Ala Tyr His Met Ile Glu Thr Tyr Gly

450

455

460

Cys Asp Tyr Ser Thr Ser Gly Leu Ser Phe Asp Thr Leu His Ser Lys

465

470

475

480

Leu Lys Ala Phe Leu Glu Leu Arg Thr Val Asp Gly Pro Arg His Asp
485 490 495

Thr Tyr Ile Leu Tyr Tyr Ser Gly His Thr His Gly Thr Gly Glu Trp
500 505 510

Ala Leu Ala Gly Gly Asp Thr Leu Arg Leu Asp Thr Leu Ile Glu Trp
515 520 525

Trp Arg Glu Lys Asn Gly Ser Phe Cys Ser Arg Leu Ile Ile Val Leu
530 535 540

Asp Ser Glu Asn Ser Thr Pro Trp Val Lys Glu Val Arg Lys Ile Asn
545 550 555 560

Asp Gln Tyr Ile Ala Val Gln Gly Ala Glu Leu Ile Lys Thr Val Asp
565 570 575

Ile Glu Glu Ala Asp Pro Pro Gln Leu Gly Asp Phe Thr Lys Asp Trp
580 585 590

Val Glu Tyr Asn Cys Asn Ser Ser Asn Asn Ile Cys Trp Thr Glu Lys
595 600 605

Gly Arg Thr Val Lys Ala Val Tyr Gly Val Ser Lys Arg Trp Ser Asp
610 615 620

Tyr Thr Leu His Leu Pro Thr Gly Ser Asp Val Ala Lys His Trp Met
625 630 635 640

Leu His Phe Pro Arg Ile Thr Tyr Pro Leu Val His Leu Ala Asn Trp
645 650 655

Leu Cys Gly Leu Asn Leu Phe Trp Ile Cys Lys Thr Cys Phe Arg Cys
660 665 670

Leu Lys Arg Leu Lys Met Ser Trp Phe Leu Pro Thr Val Leu Asp Thr
675 680 685

Gly Gln Gly Phe Lys Leu Val Lys Ser
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<210> 78

<211> 3008

<212> DNA

<213> Homo sapiens

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<222> (372).. (2462)

<400> 78

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ggcgtgccgc ctccctgttc tcagtcgcag gctgaagcct tgtctgctct cctccttttt 180

ggtttggttt tggaactgac tccgagggtt gggagagcgc gttggtagcg acggccgagt 240

cagatcacta taaacaaaat ttccacaaga gaaaatgttg aaataggagt tgcggataca 300

ttggatatac tggatgaaat acaagcgggtt aatttttgta acgtgaggga aaagcccaca 360

ttgctggtta c atg tgt aaa tca ctg cgt tat tgc ttt agt cat tgt ctc 410

Met Cys Lys Ser Leu Arg Tyr Cys Phe Ser His Cys Leu

1

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10

tat tta gca atg aca aga ctg gaa gaa gta aat aga gaa gtg aac atg 458

Tyr Leu Ala Met Thr Arg Leu Glu Glu Val Asn Arg Glu Val Asn Met

15

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25

cat tct tca gtg cgg tat ctt ggc tat tta gcc aga atc aat tta ttg 506

His Ser Ser Val Arg Tyr Leu Gly Tyr Leu Ala Arg Ile Asn Leu Leu

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35

40

45

gtt gct ata tgc tta ggt cta tac gta aga tgg gaa aaa aca gca aat 554

Val Ala Ile Cys Leu Gly Leu Tyr Val Arg Trp Glu Lys Thr Ala Asn

50

55

60

tcc tta att ttg gta att ttt att ctt ggt ctt ttt gtt ctt gga atc 602

Ser Leu Ile Leu Val Ile Phe Ile Leu Gly Leu Phe Val Leu Gly Ile

65

70

75

gcc agc ata ctc tat tac tat ttt tca atg gaa gca gca agt tta agt 650

Ala Ser Ile Leu Tyr Tyr Tyr Phe Ser Met Glu Ala Ala Ser Leu Ser

80	85	90	
c t c t c c a a t c t t t g g a t t c t t g c t t g g c c t c c t a t g t t t t c t t			698
Leu Ser Asn Leu Trp Phe Gly Phe Leu Leu Gly Leu Leu Cys Phe Leu			
95	100	105	
g a t a a t t c a t c c t t t a a a a a t g a t g t a a a g a a g a a t c a a c c a a a t a t			746
Asp Asn Ser Ser Phe Lys Asn Asp Val Lys Glu Glu Ser Thr Lys Tyr			
110	115	120	125
t t g c t t c t a a c a t c c a t a g t g t t a a g g a t a t t g t g c t c t c t g g t g g a g			794
Leu Leu Leu Thr Ser Ile Val Leu Arg Ile Leu Cys Ser Leu Val Glu			
130	135	140	
a g a a t t t c t g g t t a t g t c c g t c a t c g g c c c a c t t t a c t a a c c a c a g t t			842
Arg Ile Ser Gly Tyr Val Arg His Arg Pro Thr Leu Leu Thr Thr Val			
145	150	155	
g a a t t t c t g g a g c t t g t t g g a t t t g c c a t t g c c a g c a c a a c t a t g t t g			890
Glu Phe Leu Glu Leu Val Gly Phe Ala Ile Ala Ser Thr Thr Met Leu			
160	165	170	
g t g g a g a a g t c t c t g a g t g t c a t t t t g c t t g t t g t a g c t c t g c t a t g			938
Val Glu Lys Ser Leu Ser Val Ile Leu Leu Val Val Ala Leu Ala Met			
175	180	185	
c t g a t t a t t g a t c t g a g a a t g a a a t c t t t t a g c t a t t c c a a a c t t a			986
Leu Ile Ile Asp Leu Arg Met Lys Ser Phe Leu Ala Ile Pro Asn Leu			
190	195	200	205

gtt att ttt gca gtt ttg tta ttt ttt tcc tca ttg gaa act ccc aaa 1034

Val Ile Phe Ala Val Leu Leu Phe Phe Ser Ser Leu Glu Thr Pro Lys

210

215

220

aat ccg att gct ttt gcg tgt ttt ttt att tgc ctg ata act gat cct 1082

Asn Pro Ile Ala Phe Ala Cys Phe Phe Ile Cys Leu Ile Thr Asp Pro

225

230

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ttc ctt gac att tat ttt agt gga ctt tca gta act gaa aga tgg aaa 1130

Phe Leu Asp Ile Tyr Phe Ser Gly Leu Ser Val Thr Glu Arg Trp Lys

240

245

250

ccc ttt ttg tac cgt gga aga att tgc aga aga ctt tca gtc gtt ttt 1178

Pro Phe Leu Tyr Arg Gly Arg Ile Cys Arg Arg Leu Ser Val Val Phe

255

260

265

gct gga atg att gag ctt aca ttt ttt att ctt tcc gca ttc aaa ctt 1226

Ala Gly Met Ile Glu Leu Thr Phe Phe Ile Leu Ser Ala Phe Lys Leu

270

275

280

285

aga gac act cac ctc tgg tat ttt gta ata cct ggc ttt tcc att ttt 1274

Arg Asp Thr His Leu Trp Tyr Phe Val Ile Pro Gly Phe Ser Ile Phe

290

295

300

gga att ttc tgg atg att tgt cat att att ttt ctt tta act ctt tgg 1322

Gly Ile Phe Trp Met Ile Cys His Ile Ile Phe Leu Leu Thr Leu Trp

305

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315

gga ttc cat acc aaa tta aat gac tgc cat aaa gta tat ttt act cac 1370

Gly Phe His Thr Lys Leu Asn Asp Cys His Lys Val Tyr Phe Thr His

320

325

330

agg aca gat tac aat agc ctt gat aga atc atg gca tcc aaa ggg atg 1418

Arg Thr Asp Tyr Asn Ser Leu Asp Arg Ile Met Ala Ser Lys Gly Met

335

340

345

cgc cat ttt tgc ttg att tca gag cag ttg gtg ttc ttt agt ctt ctt 1466

Arg His Phe Cys Leu Ile Ser Glu Gln Leu Val Phe Phe Ser Leu Leu

350

355

360

365

gca aca gcg att ttg gga gca gtt tcc tgg cag cca aca aat gga att 1514

Ala Thr Ala Ile Leu Gly Ala Val Ser Trp Gln Pro Thr Asn Gly Ile

370

375

380

ttc ttg agc atg ttt cta atc gtt ttg cca ttg gaa tcc atg gct cat 1562

Phe Leu Ser Met Phe Leu Ile Val Leu Pro Leu Glu Ser Met Ala His

385

390

395

ggg ctc ttc cat gaa ttg ggt aac tgt tta gga gga aca tct gtt gga 1610

Gly Leu Phe His Glu Leu Gly Asn Cys Leu Gly Gly Thr Ser Val Gly

400

405

410

tat gct att gtg att ccc acc aac ttc tgc agt cct gat ggt cag cca 1658

Tyr Ala Ile Val Ile Pro Thr Asn Phe Cys Ser Pro Asp Gly Gln Pro

415

420

425

aca ctg ctt ccc cca gaa cat gta cag gag tta aat ttg agg tct act 1706

Thr Leu Leu Pro Pro Glu His Val Gln Glu Leu Asn Leu Arg Ser Thr
 430 435 440 445

ggc atg ctc aat gct atc caa aga ttt ttt gca tat cat atg att gag 1754
 Gly Met Leu Asn Ala Ile Gln Arg Phe Phe Ala Tyr His Met Ile Glu
 450 455 460

acc tat gga tgt gac tat tcc aca agt gga ctg tca ttt gat act ctg 1802
 Thr Tyr Gly Cys Asp Tyr Ser Thr Ser Gly Leu Ser Phe Asp Thr Leu
 465 470 475

cat tcc aaa cta aaa gct ttc ctc gaa ctt cgg aca gtg gat gga ccc 1850
 His Ser Lys Leu Lys Ala Phe Leu Glu Leu Arg Thr Val Asp Gly Pro
 480 485 490

aga cat gat acg tat att ttg tat tac agt ggg cac acc cat ggt aca 1898
 Arg His Asp Thr Tyr Ile Leu Tyr Tyr Ser Gly His Thr His Gly Thr
 495 500 505

gga gag tgg gct cta gca ggt gga gat aca cta cgc ctt gac aca ctt 1946
 Gly Glu Trp Ala Leu Ala Gly Gly Asp Thr Leu Arg Leu Asp Thr Leu
 510 515 520 525

ata gaa tgg tgg aga gaa aag aat ggt tcc ttt tgt tcc cgg ctt att 1994
 Ile Glu Trp Trp Arg Glu Lys Asn Gly Ser Phe Cys Ser Arg Leu Ile
 530 535 540

atc gta tta gac agc gaa aat tca acc cct tgg gtg aaa gaa gtg agg 2042
 Ile Val Leu Asp Ser Glu Asn Ser Thr Pro Trp Val Lys Glu Val Arg

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aaa att aat gac cag tat att gca gtg caa gga gca gag ttg ata aaa 2090

Lys Ile Asn Asp Gln Tyr Ile Ala Val Gln Gly Ala Glu Leu Ile Lys

560

565

570

aca gta gat att gaa gaa gct gac ccg cca cag cta ggt gac ttt aca 2138

Thr Val Asp Ile Glu Glu Ala Asp Pro Pro Gln Leu Gly Asp Phe Thr

575

580

585

aaa gac tgg gta gaa tat aac tgc aac tcc agt aat aac atc tgc tgg 2186

Lys Asp Trp Val Glu Tyr Asn Cys Asn Ser Ser Asn Asn Ile Cys Trp

590

595

600

605

act gaa aag gga cgc aca gtg aaa gca gta tat ggt gtg tca aaa cgg 2234

Thr Glu Lys Gly Arg Thr Val Lys Ala Val Tyr Gly Val Ser Lys Arg

610

615

620

tgg agt gac tac act ctg cat ttg cca acg gga agc gat gtg gcc aag 2282

Trp Ser Asp Tyr Thr Leu His Leu Pro Thr Gly Ser Asp Val Ala Lys

625

630

635

cac tgg atg tta cac ttt cct cgt att aca tat ccc cta gtg cat ttg 2330

His Trp Met Leu His Phe Pro Arg Ile Thr Tyr Pro Leu Val His Leu

640

645

650

gca aat tgg tta tgc ggt ctg aac ctt ttt tgg atc tgc aaa act tgt 2378

Ala Asn Trp Leu Cys Gly Leu Asn Leu Phe Trp Ile Cys Lys Thr Cys

655

660

665

ttt agg tgc ttg aaa aga tta aaa atg agt tgg ttt ctt cct act gtg 2426

Phe Arg Cys Leu Lys Arg Leu Lys Met Ser Trp Phe Leu Pro Thr Val

670

675

680

685

ctg gac aca gga caa ggc ttc aaa ctt gtc aaa tct taatttggac 2472

Leu Asp Thr Gly Gln Gly Phe Lys Leu Val Lys Ser

690

695

cccaaagcgg gatattaata agcactcata ctaccaatta tcactaactt gccatititit 2532

gtagctgta tttttatttg tggaaaatac ctgctactt ctgtagctgc tctcacttgg 2592

tcttttccta agtaattatg gtatatataa ggcgttggga aaaaacattt tataatgaaa 2652

gtagtaggg agtcaaagtc ttactgtaaa tgcataagag acgttaaaaa taacactgca 2712

ctttcaggaa tgtttgctta tggtcctgat tagaaagaaa cagttgtcta tgctctgcaa 2772

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gtagaccaga taaatttggc tactgtttta agaaaactac cagtttactt acagaagatt 2892

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<212> PRT

<213> Homo sapiens

<400> 79

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Leu Gly Leu Leu Cys Phe Leu Asp Asn Ser Ser Phe Lys Asn Asp Val

20 25 30

Lys Glu Glu Ser Thr Lys Tyr Leu Leu Leu Thr Ser Ile Val Leu Arg

35 40 45

Ile Leu Cys Ser Leu Val Glu Arg Ile Ser Gly Tyr Val Arg His Arg

50 55 60

Pro Thr Leu Leu Thr Thr Val Glu Phe Leu Glu Leu Val Gly Phe Ala

65 70 75 80

Ile Ala Ser Thr Thr Met Leu Val Glu Lys Ser Leu Ser Val Ile Leu

85 90 95

Leu Val Val Ala Leu Ala Met Leu Ile Ile Asp Leu Arg Met Lys Ser

100 105 110

Phe Leu Ala Ile Pro Asn Leu Val Ile Phe Ala Val Leu Leu Phe Phe

115 120 125

Ser Ser Leu Glu Thr Pro Lys Asn Pro Ile Ala Phe Ala Cys Phe Phe
130 135 140

Ile Cys Leu Ile Thr Asp Pro Phe Leu Asp Ile Tyr Phe Ser Gly Leu
145 150 155 160

Ser Val Thr Glu Arg Trp Lys Pro Phe Leu Tyr Arg Gly Arg Ile Cys
165 170 175

Arg Arg Leu Ser Val Val Phe Ala Gly Met Ile Glu Leu Thr Phe Phe
180 185 190

Ile Leu Ser Ala Phe Lys Leu Arg Asp Thr His Leu Trp Tyr Phe Val
195 200 205

Ile Pro Gly Phe Ser Ile Phe Gly Ile Phe Trp Met Ile Cys His Ile
210 215 220

Ile Phe Leu Leu Thr Leu Trp Gly Phe His Thr Lys Leu Asn Asp Cys
225 230 235 240

His Lys Val Tyr Phe Thr His Arg Thr Asp Tyr Asn Ser Leu Asp Arg
245 250 255

Ile Met Ala Ser Lys Gly Met Arg His Phe Cys Leu Ile Ser Glu Gln
260 265 270

Leu Val Phe Phe Ser Leu Leu Ala Thr Ala Ile Leu Gly Ala Val Ser
275 280 285

Trp Gln Pro Thr Asn Gly Ile Phe Leu Ser Met Phe Leu Ile Val Leu
290 295 300

Pro Leu Glu Ser Met Ala His Gly Leu Phe His Glu Leu Gly Asn Cys
305 310 315 320

Leu Gly Gly Thr Ser Val Gly Tyr Ala Ile Val Ile Pro Thr Asn Phe
325 330 335

Cys Ser Pro Asp Gly Gln Pro Thr Leu Leu Pro Pro Glu His Val Gln
340 345 350

Glu Leu Asn Leu Arg Ser Thr Gly Met Leu Asn Ala Ile Gln Arg Phe
355 360 365

Phe Ala Tyr His Met Ile Glu Thr Tyr Gly Cys Asp Tyr Ser Thr Ser
370 375 380

Gly Leu Ser Phe Asp Thr Leu His Ser Lys Leu Lys Ala Phe Leu Glu
385 390 395 400

Leu Arg Thr Val Asp Gly Pro Arg His Asp Thr Tyr Ile Leu Tyr Tyr
405 410 415

Ser Gly His Thr His Gly Thr Gly Glu Trp Ala Leu Ala Gly Gly Asp
420 425 430

Thr Leu Arg Leu Asp Thr Leu Ile Glu Trp Trp Arg Glu Lys Asn Gly

435	440	445
Ser Phe Cys Ser Arg Leu Ile Ile Val Leu Asp Ser Glu Asn Ser Thr		
450	455	460
Pro Trp Val Lys Glu Val Arg Lys Ile Asn Asp Gln Tyr Ile Ala Val		
465	470	475 480
Gln Gly Ala Glu Leu Ile Lys Thr Val Asp Ile Glu Glu Ala Asp Pro		
485	490	495
Pro Gln Leu Gly Asp Phe Thr Lys Asp Trp Val Glu Tyr Asn Cys Asn		
500	505	510
Ser Ser Asn Asn Ile Cys Trp Thr Glu Lys Gly Arg Thr Val Lys Ala		
515	520	525
Val Tyr Gly Val Ser Lys Arg Trp Ser Asp Tyr Thr Leu His Leu Pro		
530	535	540
Thr Gly Ser Asp Val Ala Lys His Trp Met Leu His Phe Pro Arg Ile		
545	550	555 560
Thr Tyr Pro Leu Val His Leu Ala Asn Trp Leu Cys Gly Leu Asn Leu		
565	570	575
Phe Trp Ile Cys Lys Thr Cys Phe Arg Cys Leu Lys Arg Leu Lys Met		
580	585	590

Ser Trp Phe Leu Pro Thr Val Leu Asp Thr Gly Gln Gly Phe Lys Leu
595 600 605

Val Lys Ser
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<210> 80

<211> 3007

<212> DNA

<213> Homo sapiens

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ggcgtgccgc cccccgttc tcagtcgcag gctgaagcct tgtctgctct cctccitttt 180

ggtttggttt tggaactgac tccgaggggt gggagagcgc gttggtggcg acggccgagt 240

cagatcacta taaacaaaat ttccacaaga gaaaatgttg aaataggagt tgcggataca 300

ttggatatac tggatgaaat acaagcgggt aatttttgta acgtgaggga aaagcccaca 360

ttgctggta caigtgtaaa tcactgcgtt attgctttag tcattgtctc tatttagcaa 420

tgacaagact ggaagaagta aatagagaag tgaacatgca ttcttcagtg cggatatctg 480

ctatttagcc agaatcaatt tattggttgc tataatgctta ggtctatacg taagatggga 540

aaaaacagca aattccttaa ttttggtaat ttttattctt ggtctttttg ttcttggaat 600

cgccagcata ctctattact atttttca atg gaa gca gca agt tta agt ctc 652

Met Glu Ala Ala Ser Leu Ser Leu

1

5

tcc aat ctt tgg ttt gga ttc ttg ctt ggc ctc cta tgt ttt ctt gat 700

Ser Asn Leu Trp Phe Gly Phe Leu Leu Gly Leu Leu Cys Phe Leu Asp

10

15

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aat tca tcc ttt aaa aat gat gta aaa gaa gaa tca acc aaa tat ttg 748

Asn Ser Ser Phe Lys Asn Asp Val Lys Glu Glu Ser Thr Lys Tyr Leu

25

30

35

40

ctt cta aca tcc ata gtg tta agg ata ttg tgc tct ctg gtg gag aga 796

Leu Leu Thr Ser Ile Val Leu Arg Ile Leu Cys Ser Leu Val Glu Arg

45

50

55

att tct ggt tat gtc cgt cat cgg ccc act tta cta acc aca gtt gaa 844

Ile Ser Gly Tyr Val Arg His Arg Pro Thr Leu Leu Thr Thr Val Glu

60

65

70

ttt ctg gag ctt gtt gga ttt gcc att gcc agc aca act atg ttg gtg 892

Phe Leu Glu Leu Val Gly Phe Ala Ile Ala Ser Thr Thr Met Leu Val

75

80

85

gag aag tct ctg agt gtc att ttg ctt gtt gta gct ctg gct atg ctg 940

Glu Lys Ser Leu Ser Val Ile Leu Leu Val Val Ala Leu Ala Met Leu

90

95

100

att att gat ctg aga atg aaa tct ttc tta gct att cca aac tta gtt 988

Ile Ile Asp Leu Arg Met Lys Ser Phe Leu Ala Ile Pro Asn Leu Val

105

110

115

120

att ttt gca gtt ttg tta ttt ttt tcc tca ttg gaa act ccc aaa aat 1036

Ile Phe Ala Val Leu Leu Phe Phe Ser Ser Leu Glu Thr Pro Lys Asn

125

130

135

ccg att gct ttt gcg tgt ttt ttt att tgc ctg ata act gat cct ttc 1084

Pro Ile Ala Phe Ala Cys Phe Phe Ile Cys Leu Ile Thr Asp Pro Phe

140

145

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ctt gac att tat ttt agt gga ctt tca gla act gaa aga tgg aaa ccc 1132

Leu Asp Ile Tyr Phe Ser Gly Leu Ser Val Thr Glu Arg Trp Lys Pro

155

160

165

ttt ttg tac cgt gga aga att tgc aga aga ctt tca gtc gtt ttt gct 1180

Phe Leu Tyr Arg Gly Arg Ile Cys Arg Arg Leu Ser Val Val Phe Ala

170

175

180

gga atg att gag ctt aca ttt ttt att ctt tcc gca ttc aaa ctt aga 1228

Gly Met Ile Glu Leu Thr Phe Phe Ile Leu Ser Ala Phe Lys Leu Arg

185	190	195	200	
gac act cac ctc tgg tat ttt gta ata cct ggc ttt tcc att ttt gga				1276
Asp Thr His Leu Trp Tyr Phe Val Ile Pro Gly Phe Ser Ile Phe Gly				
	205	210	215	
att ttc tgg atg att tgt cat att att ttt ctt tta act ctt tgg gga				1324
Ile Phe Trp Met Ile Cys His Ile Ile Phe Leu Leu Thr Leu Trp Gly				
	220	225	230	
ttc cat acc aaa tta aat gac tgc cat aaa gta tat ttt act cac agg				1372
Phe His Thr Lys Leu Asn Asp Cys His Lys Val Tyr Phe Thr His Arg				
	235	240	245	
aca gat tac aat agc ctt gat aga atc atg gca tcc aaa ggg atg cgc				1420
Thr Asp Tyr Asn Ser Leu Asp Arg Ile Met Ala Ser Lys Gly Met Arg				
	250	255	260	
cat ttt tgc ttg att tca gag cag ttg gtg ttc ttt agt ctt ctt gca				1468
His Phe Cys Leu Ile Ser Glu Gln Leu Val Phe Phe Ser Leu Leu Ala				
265	270	275	280	
aca gcg att ttg gga gca gtt tcc tgg cag cca aca aat gga att ttc				1516
Thr Ala Ile Leu Gly Ala Val Ser Trp Gln Pro Thr Asn Gly Ile Phe				
	285	290	295	
ttg agc atg ttt cta atc gtt ttg cca ttg gaa tcc atg gcl cat ggg				1564
Leu Ser Met Phe Leu Ile Val Leu Pro Leu Glu Ser Met Ala His Gly				
300	305	310		

ctc ttc cat gaa ttg ggt aac tgt tta gga gga aca tct gtt gga tat 1612

Leu Phe His Glu Leu Gly Asn Cys Leu Gly Gly Thr Ser Val Gly Tyr

315

320

325

gct att gtg att ccc acc aac ttc tgc agt cct gat ggt cag cca aca 1660

Ala Ile Val Ile Pro Thr Asn Phe Cys Ser Pro Asp Gly Gln Pro Thr

330

335

340

ctg ctt ccc cca gaa cat gta cag gag tta aat ttg agg tct act ggc 1708

Leu Leu Pro Pro Glu His Val Gln Glu Leu Asn Leu Arg Ser Thr Gly

345

350

355

360

atg ctc aat gct atc caa aga ttt ttt gca tat cat atg att gag acc 1756

Met Leu Asn Ala Ile Gln Arg Phe Phe Ala Tyr His Met Ile Glu Thr

365

370

375

tat gga tgt gac tat tcc aca agt gga ctg tca ttt gat act ctg cat 1804

Tyr Gly Cys Asp Tyr Ser Thr Ser Gly Leu Ser Phe Asp Thr Leu His

380

385

390

tcc aaa cta aaa gct ttc ctc gaa ctt cgg aca gtg gat gga ccc aga 1852

Ser Lys Leu Lys Ala Phe Leu Glu Leu Arg Thr Val Asp Gly Pro Arg

395

400

405

cat gat acg tat att ttg tat tac agt ggg cac acc cat ggt aca gga 1900

His Asp Thr Tyr Ile Leu Tyr Tyr Ser Gly His Thr His Gly Thr Gly

410

415

420

gag tgg gct cta gca ggt gga gat aca cta cgc ctt gac aca ctt ata 1948
 Glu Trp Ala Leu Ala Gly Gly Asp Thr Leu Arg Leu Asp Thr Leu Ile
 425 430 435 440

gaa tgg tgg aga gaa aag aat ggt tcc ttt tgt tcc cgg ctt att atc 1996
 Glu Trp Trp Arg Glu Lys Asn Gly Ser Phe Cys Ser Arg Leu Ile Ile
 445 450 455

gta tta gac agc gaa aat tca acc cct tgg gtg aaa gaa gtg agg aaa 2044
 Val Leu Asp Ser Glu Asn Ser Thr Pro Trp Val Lys Glu Val Arg Lys
 460 465 470

att aat gac cag tat att gca gtg caa gga gca gag ttg ata aaa aca 2092
 Ile Asn Asp Gln Tyr Ile Ala Val Gln Gly Ala Glu Leu Ile Lys Thr
 475 480 485

gta gat att gaa gaa gct gac ccg cca cag cta ggt gac ttt aca aaa 2140
 Val Asp Ile Glu Glu Ala Asp Pro Pro Gln Leu Gly Asp Phe Thr Lys
 490 495 500

gac tgg gta gaa tat aac tgc aac tcc agt aat aac atc tgc tgg act 2188
 Asp Trp Val Glu Tyr Asn Cys Asn Ser Ser Asn Asn Ile Cys Trp Thr
 505 510 515 520

gaa aag gga cgc aca gtg aaa gca gla tat ggt gtg tca aaa cgg tgg 2236
 Glu Lys Gly Arg Thr Val Lys Ala Val Tyr Gly Val Ser Lys Arg Trp
 525 530 535

agt gac tac act ctg cat ttg cca acg gga agc gat gtg gcc aag cac 2284

Ser Asp Tyr Thr Leu His Leu Pro Thr Gly Ser Asp Val Ala Lys His
540 545 550

tgg atg tta cac ttt cct cgt att aca tat ccc cta gtg cat ttg gca 2332
Trp Met Leu His Phe Pro Arg Ile Thr Tyr Pro Leu Val His Leu Ala
555 560 565

aat tgg tta tgc ggt ctg aac ctt ttt tgg atc tgc aaa act tgt ttt 2380
Asn Trp Leu Cys Gly Leu Asn Leu Phe Trp Ile Cys Lys Thr Cys Phe
570 575 580

agg tgc ttg aaa aga tta aaa atg agt tgg ttt ctt cct act gtg ctg 2428
Arg Cys Leu Lys Arg Leu Lys Met Ser Trp Phe Leu Pro Thr Val Leu
585 590 595 600

gac aca gga caa ggc ttc aaa ctt gtc aaa tct taatttggac cccaaagcgg 2481
Asp Thr Gly Gln Gly Phe Lys Leu Val Lys Ser
605 610

gatattaata agcactcata ctaccaatta tcactaactt gccatttttt gtatgctgta 2541

tttttatttg tggaaaatac ctgtctactt ctgtagctgc tctcactttg tcttttctta 2601

agtaattatg gtatatataa ggcgttggga aaaaacattt tataatgaaa gtatgtaggg 2661

agicaaatgc ttactgtaaa tgcataagag acgttaaaaa taacactgca ctttcaggaa 2721

tgtttgctta tggctctgat tagaaagaaa cagttgtcta tgctctgcaa tggatcaatga 2781

tgaattacta atgccttatt ttctaggcat ataataatag tttagagaat gtagaccaga 2841

taaatttgtt tactgtttta agaaaactac cagtttactt acagaagatt cttttttcca 2901

aacagtaggt ttcatccaag accatttgaa gaactgcaaa ctctttctct tagaaaagaa 2961

agagggcagc ctaaaataaa cgcaaaattt gcttatactc catcac 3007

<210> 81

<211> 184

<212> PRT

<213> Homo sapiens

<400> 81

Met Thr Ser Phe Glu Asp Ala Asp Thr Glu Glu Thr Val Thr Cys Leu

1 5 10 15

Gln Met Thr Val Tyr His Pro Gly Gln Leu Gln Cys Gly Ile Phe Gln

20 25 30

Ser Ile Ser Phe Asn Arg Glu Lys Leu Pro Ser Ser Glu Val Val Lys

35 40 45

Phe Gly Arg Asn Ser Asn Ile Cys His Tyr Thr Phe Gln Asp Lys Gln

50 55 60

Val Ser Arg Val Gln Phe Ser Leu Gln Leu Phe Lys Lys Phe Asn Ser

65 70 75 80

Ser Val Leu Ser Phe Glu Ile Lys Asn Met Ser Lys Lys Thr Asn Leu

85

90

95

Ile Val Asp Ser Arg Glu Leu Gly Tyr Leu Asn Lys Met Asp Leu Pro

100

105

110

Tyr Arg Cys Met Val Arg Phe Gly Glu Tyr Gln Phe Leu Met Glu Lys

115

120

125

Glu Asp Gly Glu Ser Leu Glu Phe Phe Glu Thr Gln Phe Ile Leu Ser

130

135

140

Pro Arg Ser Leu Leu Gln Glu Asn Asn Trp Pro Pro His Arg Pro Ile

145

150

155

160

Pro Glu Tyr Gly Thr Tyr Ser Leu Cys Ser Ser Gln Ser Ser Ser Pro

165

170

175

Thr Glu Met Asp Glu Asn Glu Ser

180

<210> 82

<211> 1617

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (285).. (836)

<400> 82

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gcgcgcgcgg gagcgcggga ggatcggcgg ctgcgggtca ctggccccg gctcgggtcc 120

ccgcaccccg gggtcacac ttacccgcgc ggaggagcag cggccgggtg tccaccccca 180

tcctgcgcc agtctctctg attccccctg ctctgagccg ggagagccga acagctgaag 240

agagttcact gactccccag ccccagggtg gccttgtgca catc atg acc agt ttt 296

Met Thr Ser Phe

1

gaa gat gct gac aca gaa gag aca gta act tgt ctc cag atg acg gtt 344

Glu Asp Ala Asp Thr Glu Glu Thr Val Thr Cys Leu Gln Met Thr Val

5

10

15

20

tac cat cct ggc cag ttg cag tgt gga ata ttt cag tca ata agt ttt 392

Tyr His Pro Gly Gln Leu Gln Cys Gly Ile Phe Gln Ser Ile Ser Phe

25

30

35

aac aga gag aaa ctc cct tcc agc gaa gtg gtg aaa ttt ggc cga aat 440

Asn Arg Glu Lys Leu Pro Ser Ser Glu Val Val Lys Phe Gly Arg Asn

40

45

50

tcc aac atc tgt cat tat act ttt cag gac aaa cag gtt tcc cga gtt 488

Ser Asn Ile Cys His Tyr Thr Phe Gln Asp Lys Gln Val Ser Arg Val

55

60

65

cag ttt tct ctg cag ctg ttt aaa aaa ttc aac agc tca gtt ctc tcc 536

Gln Phe Ser Leu Gln Leu Phe Lys Lys Phe Asn Ser Ser Val Leu Ser

70

75

80

ttt gaa ata aaa aat atg agt aaa aag acc aat ctg atc gtg gac agc 584

Phe Glu Ile Lys Asn Met Ser Lys Lys Thr Asn Leu Ile Val Asp Ser

85

90

95

100

aga gag ctg ggc tac cta aat aaa atg gac ctg cca tac agg tgc atg 632

Arg Glu Leu Gly Tyr Leu Asn Lys Met Asp Leu Pro Tyr Arg Cys Met

105

110

115

gtc aga ttc gga gag tat cag ttt ctg atg gag aag gaa gat ggc gag 680

Val Arg Phe Gly Glu Tyr Gln Phe Leu Met Glu Lys Glu Asp Gly Glu

120

125

130

tca ttg gaa ttt ttt gag act caa ttt att tta tct cca aga tca ctc 728

Ser Leu Glu Phe Phe Glu Thr Gln Phe Ile Leu Ser Pro Arg Ser Leu

135

140

145

ttg caa gaa aac aac tgg cca cca cac agg ccc ata ccg gag tat ggc 776

Leu Gln Glu Asn Asn Trp Pro Pro His Arg Pro Ile Pro Glu Tyr Gly

150

155

160

act tat tgc ctc tgc tcc tcc caa agc agt tct ccg aca gaa atg gat 824

Thr Tyr Ser Leu Cys Ser Ser Gln Ser Ser Ser Pro Thr Glu Met Asp

165

170

175

180

gaa aat gag tca tgaacacaga aagtctaaga ggagaaatat gatggatgaa 876

Glu Asn Glu Ser

gagctctgta gatgctgtat agacactaaa taagagtga ttagggtagt atattatagt 936

catctgttat gctgtgaaat ttggaattca gtattatcat ttggaagtct gtaaattgtg 996

ttagtcatta acttagtcac ctgttgtatt ctggatctac acaaaattat tttaactgct 1056

cttattaatc tgtgaggait aatatacaaa aagtatccit tgagatgaag tcgtgttctc 1116

aaaataaggt tatattatit tctttttctg cttgattttc atcttgtgtt ttgctttgtt 1176

tttgtaagga accatctctt ggtttggtea catcagttca caacagccat ttgttttcaa 1236

ggteaaggct ccaggcaggt tgttactggt gtttgcagcc tgtcagtact tgcagttactg 1296

gaataggttc taggctagtg tctgcgcgtc actgtggitt tagcatggga ggacttatit 1356

gagaaatact accttacttt tctatgattt ctttttacag agttatagtg tgtttactcc 1416

taagatgaca gtctctttg tctatattca gcactaaga caaatattta aacattttta 1476

agaaccactg tgttaagttt aggattatit acttaccaaa ttagaagttt gacttttatg 1536

tgttatacac aatcttaaaa ttfcacgaat tcacctttit aatagtatcc atgtacataa 1596

taaaatcaaa gtttaattag c

1617

<210> 83

<211> 392

<212> PRT

<213> Homo sapiens

<400> 83

Met Asp Ala Arg Trp Trp Ala Val Val Val Leu Ala Ala Phe Pro Ser

1

5

10

15

Leu Gly Ala Gly Gly Glu Thr Pro Glu Ala Pro Pro Glu Ser Trp Thr

20

25

30

Gln Leu Trp Phe Phe Arg Phe Val Val Asn Ala Ala Gly Tyr Ala Ser

35

40

45

Phe Met Val Pro Gly Tyr Leu Leu Val Gln Tyr Phe Arg Arg Lys Asn

50

55

60

Tyr Leu Glu Thr Gly Arg Gly Leu Cys Phe Pro Leu Val Lys Ala Cys

65

70

75

80

Val Phe Gly Asn Glu Pro Lys Ala Ser Asp Glu Val Pro Leu Ala Pro

85

90

95

Arg Thr Glu Ala Ala Glu Thr Thr Pro Met Trp Gln Ala Leu Lys Leu

100

105

110

Leu Phe Cys Ala Thr Gly Leu Gln Val Ser Tyr Leu Thr Trp Gly Val
115 120 125

Leu Gln Glu Arg Val Met Thr Arg Ser Tyr Gly Ala Thr Ala Thr Ser
130 135 140

Pro Gly Glu Arg Phe Thr Asp Ser Gln Phe Leu Val Leu Met Asn Arg
145 150 155 160

Val Leu Ala Leu Ile Val Ala Gly Leu Ser Cys Val Leu Cys Lys Gln
165 170 175

Pro Arg His Gly Ala Pro Met Tyr Arg Tyr Ser Phe Ala Ser Leu Ser
180 185 190

Asn Val Leu Ser Ser Trp Cys Gln Tyr Glu Ala Leu Lys Phe Val Ser
195 200 205

Phe Pro Thr Gln Val Leu Ala Lys Ala Ser Lys Val Ile Pro Val Met
210 215 220

Leu Met Gly Lys Leu Val Ser Arg Arg Ser Tyr Glu His Trp Glu Tyr
225 230 235 240

Leu Thr Ala Thr Leu Ile Ser Ile Gly Val Ser Met Phe Leu Leu Ser
245 250 255

Ser Gly Pro Glu Pro Arg Ser Ser Pro Ala Thr Thr Leu Ser Gly Leu

260

265

270

Phe Thr Val Gly Ser Leu Leu Glu Gln Gly Ala Leu Leu Glu Gly Thr

275

280

285

Arg Phe Met Gly Arg His Ser Glu Phe Ala Ala His Ala Leu Leu Leu

290

295

300

Ser Ile Cys Ser Ala Cys Gly Gln Leu Phe Ile Phe Tyr Thr Ile Gly

305

310

315

320

Gln Phe Gly Ala Ala Val Phe Thr Ile Ile Met Thr Leu Arg Gln Ala

325

330

335

Phe Ala Ile Leu Leu Ser Cys Leu Leu Tyr Gly His Thr Val Thr Val

340

345

350

Val Gly Gly Leu Gly Val Ala Val Val Phe Ala Ala Leu Leu Leu Arg

355

360

365

Val Tyr Ala Arg Gly Arg Leu Lys Gln Arg Gly Lys Lys Ala Val Pro

370

375

380

Val Glu Ser Pro Val Gln Lys Val

385

390

<210> 84

<211> 1898

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (119).. (1294)

<400> 84

acttccgctg gccgctggct cgctggccgc tccaggaggc ggccggcggga gcgcaggggg 60

cgccggccc ggggactcgc atccccggt tccccctcca cccacgcgg cctggacc 118

atg gac gcc aga tgg tgg gca gtg gtg gtg ctg gct gcg ttc ccc tcc 166

Met Asp Ala Arg Trp Trp Ala Val Val Val Leu Ala Ala Phe Pro Ser

1

5

10

15

cta ggg gca ggt ggg gag act ccc gaa gcc cct ccg gag tca tgg acc 214

Leu Gly Ala Gly Gly Glu Thr Pro Glu Ala Pro Pro Glu Ser Trp Thr

20

25

30

cag cta tgg ttc ttc cga ttt gtg gtg aat gct gct ggc tat gcc agc 262

Gln Leu Trp Phe Phe Arg Phe Val Val Asn Ala Ala Gly Tyr Ala Ser

35

40

45

ttt atg gta cct ggc tac ctc ctg gtg cag tac ttc agg cgg aag aac 310

Phe Met Val Pro Gly Tyr Leu Leu Val Gln Tyr Phe Arg Arg Lys Asn

50

55

60

tac ctg gag acc ggt agg ggc ctc tgc ttt ccc ctg gtg aaa gct tgt 358

Tyr Leu Glu Thr Gly Arg Gly Leu Cys Phe Pro Leu Val Lys Ala Cys
 65 70 75 80

gtg ttt ggc aat gag ccc aag gcc tct gat gag gtt ccc ctg gcg ccc 406
 Val Phe Gly Asn Glu Pro Lys Ala Ser Asp Glu Val Pro Leu Ala Pro
 85 90 95

cga aca gag gcg gca gag acc acc ccg atg tgg cag gcc ctg aag ctg 454
 Arg Thr Glu Ala Ala Glu Thr Thr Pro Met Trp Gln Ala Leu Lys Leu
 100 105 110

ctc ttc tgt gcc aca ggg ctc cag gtg tct tat ctg act tgg ggt gtg 502
 Leu Phe Cys Ala Thr Gly Leu Gln Val Ser Tyr Leu Thr Trp Gly Val
 115 120 125

ctg cag gaa aga gtg atg acc cgc agc tat ggg gcc aca gcc aca tca 550
 Leu Gln Glu Arg Val Met Thr Arg Ser Tyr Gly Ala Thr Ala Thr Ser
 130 135 140

ccg ggt gag cgc ttt acg gac tcg cag ttc ctg gtg cta atg aac cga 598
 Pro Gly Glu Arg Phe Thr Asp Ser Gln Phe Leu Val Leu Met Asn Arg
 145 150 155 160

gtg ctg gca ctg att gtg gct ggc ctc tcc tgt gtt ctc tgc aag cag 646
 Val Leu Ala Leu Ile Val Ala Gly Leu Ser Cys Val Leu Cys Lys Gln
 165 170 175

ccc cgg cat ggg gca ccc atg tac cgg tac tcc ttt gcc agc ctg tcc 694
 Pro Arg His Gly Ala Pro Met Tyr Arg Tyr Ser Phe Ala Ser Leu Ser

180

185

190

aat gtg ctt agc agc tgg tgc caa tac gaa gct ctt aag ttc gtc agc 742

Asn Val Leu Ser Ser Trp Cys Gln Tyr Glu Ala Leu Lys Phe Val Ser

195

200

205

ttc ccc acc cag gtg ctg gcc aag gcc tct aag gtg atc cct gtc atg 790

Phe Pro Thr Gln Val Leu Ala Lys Ala Ser Lys Val Ile Pro Val Met

210

215

220

ctg atg gga aag ctt gtg tct cgg cgc agc tac gaa cac tgg gag tac 838

Leu Met Gly Lys Leu Val Ser Arg Arg Ser Tyr Glu His Trp Glu Tyr

225

230

235

240

ctg aca gcc acc ctc atc tcc att ggg gtc agc atg ttt ctg cta tcc 886

Leu Thr Ala Thr Leu Ile Ser Ile Gly Val Ser Met Phe Leu Leu Ser

245

250

255

agc gga cca gag ccc cgc agc tcc cca gcc acc aca ctc tca ggc ctc 934

Ser Gly Pro Glu Pro Arg Ser Ser Pro Ala Thr Thr Leu Ser Gly Leu

260

265

270

ttc aca gtg ggc tca ctg cta gaa cag ggg gcc cta ctg gag gga acc 982

Phe Thr Val Gly Ser Leu Leu Glu Gln Gly Ala Leu Leu Glu Gly Thr

275

280

285

cgc ttc atg ggg cga cac agt gag ttt gct gcc cat gcc ctg cta ctc 1030

Arg Phe Met Gly Arg His Ser Glu Phe Ala Ala His Ala Leu Leu Leu

290

295

300

tcc atc tgc tcc gca tgt ggc cag ctc ttc atc ttt tac acc att ggg 1078
Ser Ile Cys Ser Ala Cys Gly Gln Leu Phe Ile Phe Tyr Thr Ile Gly
305 310 315 320

cag ttt ggg gct gcc gtc ttc acc atc atc atg acc ctc cgc cag gcc 1126
Gln Phe Gly Ala Ala Val Phe Thr Ile Ile Met Thr Leu Arg Gln Ala
325 330 335

ttt gcc atc ctt ctt tcc tgc ctt ctc tat ggc cac act gtc act gtg 1174
Phe Ala Ile Leu Leu Ser Cys Leu Leu Tyr Gly His Thr Val Thr Val
340 345 350

gtg gga ggg ctc ggg gtg gct gtg gtc ttt gct gcc ctc ctg ctc aga 1222
Val Gly Gly Leu Gly Val Ala Val Val Phe Ala Ala Leu Leu Leu Arg
355 360 365

gtc tac gcg cgg ggc cgt cta aag caa cgg gga aag aag gct gtg cct 1270
Val Tyr Ala Arg Gly Arg Leu Lys Gln Arg Gly Lys Lys Ala Val Pro
370 375 380

gtt gag tct cct gtg cag aag gtt tgagggtgga aagggcctga ggggtgaagt 1324
Val Glu Ser Pro Val Gln Lys Val
385 390

gaaataggac cctcccacca tccccttctg ctgtaacctc tgaggagct ggctgaaagg 1384

gcaaaatgca ggtgttttct cagtatcaca gaccagctct gcagcagggg attggggagc 1444

ccaggaggca gccitccctt ttgccttaag tcacccatct tccagtaagc agtttattct 1504

gagccccggg gglagacagt cctcagtgag gggttttggg gagtttggg tcaagagagc 1564

ataggttagt tccacagtta ctcttccac aagttccctt aagicttgcc cttagctgtc 1624

tctgccacct tccagactca ctccctctg caaatacctg catttcttac cctggtgaga 1684

aaagcacaag cgggttaggc tccaatgctg ctttcccagg agggatgaaga tggctgtgtg 1744

ctgaggaaag gggatgcaga gccctgccca gcaccaccac ctctatgct cctggatccc 1804

taggctctgt tccatgagcc tgttgaggt tttggtactt tagaaatgta actttttgct 1864

cttataattt tattttatta aattaaatta ctgc 1898

<210> 85

<211> 432

<212> PRT

<213> Homo sapiens

<400> 85

Met Asp Ala Arg Trp Trp Ala Val Val Val Leu Ala Ala Phe Pro Ser

1

5

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15

Leu Gly Ala Gly Gly Glu Thr Pro Glu Ala Pro Pro Glu Ser Trp Thr

20

25

30

Gln Leu Trp Phe Phe Arg Phe Val Val Asn Ala Ala Gly Tyr Ala Ser
35 40 45

Phe Met Val Pro Gly Tyr Leu Leu Val Gln Tyr Phe Arg Arg Lys Asn
50 55 60

Tyr Leu Glu Thr Gly Arg Gly Leu Cys Phe Pro Leu Val Lys Ala Cys
65 70 75 80

Val Phe Gly Asn Glu Pro Lys Ala Ser Asp Glu Val Pro Leu Ala Pro
85 90 95

Arg Thr Glu Ala Ala Glu Thr Thr Pro Met Trp Gln Ala Leu Lys Leu
100 105 110

Leu Phe Cys Ala Thr Gly Leu Gln Val Ser Tyr Leu Thr Trp Gly Val
115 120 125

Leu Gln Glu Arg Val Met Thr Arg Ser Tyr Gly Ala Thr Ala Thr Ser
130 135 140

Pro Gly Glu Arg Phe Thr Asp Ser Gln Phe Leu Val Leu Met Asn Arg
145 150 155 160

Val Leu Ala Leu Ile Val Ala Gly Leu Ser Cys Val Leu Cys Lys Gln
165 170 175

Pro Arg His Gly Ala Pro Met Tyr Arg Tyr Ser Phe Ala Ser Leu Ser
180 185 190

Asn Val Leu Ser Ser Trp Cys Gln Tyr Glu Ala Leu Lys Phe Val Ser
195 200 205

Phe Pro Thr Gln Val Leu Ala Lys Ala Ser Lys Val Ile Pro Val Met
210 215 220

Leu Met Gly Lys Leu Val Ser Arg Arg Ser Tyr Glu His Trp Glu Tyr
225 230 235 240

Leu Thr Ala Thr Leu Ile Ser Ile Gly Val Ser Met Phe Leu Leu Ser
245 250 255

Ser Gly Pro Glu Pro Arg Ser Ser Pro Ala Thr Thr Leu Ser Gly Leu
260 265 270

Ile Leu Leu Ala Gly Tyr Ile Ala Phe Asp Ser Phe Thr Ser Asn Trp
275 280 285

Gln Asp Ala Leu Phe Ala Tyr Lys Met Ser Ser Val Gln Met Met Phe
290 295 300

Gly Val Asn Phe Phe Ser Cys Leu Phe Thr Val Gly Ser Leu Leu Glu
305 310 315 320

Gln Gly Ala Leu Leu Glu Gly Thr Arg Phe Met Gly Arg His Ser Glu
325 330 335

Phe Ala Ala His Ala Leu Leu Leu Ser Ile Cys Ser Ala Cys Gly Gln

340

345

350

Leu Phe Ile Phe Tyr Thr Ile Gly Gln Phe Gly Ala Ala Val Phe Thr

355

360

365

Ile Ile Met Thr Leu Arg Gln Ala Phe Ala Ile Leu Leu Ser Cys Leu

370

375

380

Leu Tyr Gly His Thr Val Thr Val Val Gly Gly Leu Gly Val Ala Val

385

390

395

400

Val Phe Ala Ala Leu Leu Leu Arg Val Tyr Ala Arg Gly Arg Leu Lys

405

410

415

Gln Arg Gly Lys Lys Ala Val Pro Val Glu Ser Pro Val Gln Lys Val

420

425

430

<210> 86

<211> 2018

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (119).. (1414)

<400> 86

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cgcgcgcccc ggggactcgc attccccggt tccccctcca cccacgcgg cctggacc 118

atg gac gcc aga tgg tgg gca gtg gtg gtg ctg gct gcg ttc ccc tcc 166

Met Asp Ala Arg Trp Trp Ala Val Val Val Leu Ala Ala Phe Pro Ser

1 5 10 15

cta ggg gca ggt ggg gag act ccc gaa gcc cct ccg gag tca tgg acc 214

Leu Gly Ala Gly Gly Glu Thr Pro Glu Ala Pro Pro Glu Ser Trp Thr

20 25 30

cag cta tgg ttc ttc cga ttt gtg gtg aat gct gct ggc tat gcc agc 262

Gln Leu Trp Phe Phe Arg Phe Val Val Asn Ala Ala Gly Tyr Ala Ser

35 40 45

ttt atg gta cct ggc tac ctc ctg gtg cag tac ttc agg cgg aag aac 310

Phe Met Val Pro Gly Tyr Leu Leu Val Gln Tyr Phe Arg Arg Lys Asn

50 55 60

tac ctg gag acc ggt agg ggc ctc tgc ttt ccc ctg gtg aaa gct tgt 358

Tyr Leu Glu Thr Gly Arg Gly Leu Cys Phe Pro Leu Val Lys Ala Cys

65 70 75 80

gtg ttt ggc aat gag ccc aag gcc tct gat gag gtt ccc ctg gcg ccc 406

Val Phe Gly Asn Glu Pro Lys Ala Ser Asp Glu Val Pro Leu Ala Pro

85 90 95

cga aca gag gcg gca gag acc acc ccg atg tgg cag gcc ctg aag ctg 454

Arg Thr Glu Ala Ala Glu Thr Thr Pro Met Trp Gln Ala Leu Lys Leu

100

105

110

ctc ttc tgt gcc aca ggg ctc cag gtg tct tat ctg act tgg ggt gtg 502

Leu Phe Cys Ala Thr Gly Leu Gln Val Ser Tyr Leu Thr Trp Gly Val

115

120

125

ctg cag gaa aga gtg atg acc cgc agc tat ggg gcc aca gcc aca tca 550

Leu Gln Glu Arg Val Met Thr Arg Ser Tyr Gly Ala Thr Ala Thr Ser

130

135

140

ccg ggt gag cgc ttt acg gac tgc cag ttc ctg gtg cta atg aac cga 598

Pro Gly Glu Arg Phe Thr Asp Ser Gln Phe Leu Val Leu Met Asn Arg

145

150

155

160

gtg ctg gca ctg att gtg gct ggc ctc tcc tgt gtt ctc tgc aag cag 646

Val Leu Ala Leu Ile Val Ala Gly Leu Ser Cys Val Leu Cys Lys Gln

165

170

175

ccc cgg cat ggg gca ccc atg tac cgg tac tcc ttt gcc agc ctg tcc 694

Pro Arg His Gly Ala Pro Met Tyr Arg Tyr Ser Phe Ala Ser Leu Ser

180

185

190

aat gtg ctt agc agc tgg tgc caa tac gaa gct ctt aag ttc gtc agc 742

Asn Val Leu Ser Ser Trp Cys Gln Tyr Glu Ala Leu Lys Phe Val Ser

195

200

205

ttc ccc acc cag gtg ctg gcc aag gcc tct aag gtg atc cct gtc atg 790

Phe Pro Thr Gln Val Leu Ala Lys Ala Ser Lys Val Ile Pro Val Met

210

215

220

ctg atg gga aag ctt gtg tct cgg cgc agc tac gaa cac tgg gag tac 838

Leu Met Gly Lys Leu Val Ser Arg Arg Ser Tyr Glu His Trp Glu Tyr

225

230

235

240

ctg aca gcc acc ctc atc tcc att ggg gtc agc atg ttt ctg cta tcc 886

Leu Thr Ala Thr Leu Ile Ser Ile Gly Val Ser Met Phe Leu Leu Ser

245

250

255

agc gga cca gag ccc cgc agc tcc cca gcc acc aca ctc tca ggc ctc 934

Ser Gly Pro Glu Pro Arg Ser Ser Pro Ala Thr Thr Leu Ser Gly Leu

260

265

270

atc tta ctg gca ggt tat att gct ttt gac agc ttc acc tca aac tgg 982

Ile Leu Leu Ala Gly Tyr Ile Ala Phe Asp Ser Phe Thr Ser Asn Trp

275

280

285

cag gat gcc ctg ttt gcc tat aag atg tca tgc gtg cag atg atg ttt 1030

Gln Asp Ala Leu Phe Ala Tyr Lys Met Ser Ser Val Gln Met Met Phe

290

295

300

ggg gtc aat ttc ttc tcc tgc ctc ttc aca gtg ggc tca ctg cta gaa 1078

Gly Val Asn Phe Phe Ser Cys Leu Phe Thr Val Gly Ser Leu Leu Glu

305

310

315

320

cag ggg gcc cta ctg gag gga acc cgc ttc atg ggg cga cac agt gag 1126

Gln Gly Ala Leu Leu Glu Gly Thr Arg Phe Met Gly Arg His Ser Glu

325

330

335

ttt gct gcc cat gcc ctg cta ctc tcc atc tgc tcc gca tgt ggc cag 1174
 Phe Ala Ala His Ala Leu Leu Leu Ser Ile Cys Ser Ala Cys Gly Gln

340

345

350

ctc ttc atc ttt tac acc att ggg cag ttt ggg gct gcc gtc ttc acc 1222
 Leu Phe Ile Phe Tyr Thr Ile Gly Gln Phe Gly Ala Ala Val Phe Thr

355

360

365

atc atc atg acc ctc cgc cag gcc ttt gcc atc ctt ctt tcc tgc ctt 1270
 Ile Ile Met Thr Leu Arg Gln Ala Phe Ala Ile Leu Leu Ser Cys Leu

370

375

380

ctc tat ggc cac act gtc act gtg gtg gga ggg ctg ggg gtg gct gtg 1318
 Leu Tyr Gly His Thr Val Thr Val Val Gly Gly Leu Gly Val Ala Val
 385 390 395 400

gtc ttt gct gcc ctc ctg ctc aga gtc tac gcg cgg ggc cgt cta aag 1366
 Val Phe Ala Ala Leu Leu Leu Arg Val Tyr Ala Arg Gly Arg Leu Lys

405

410

415

caa cgg gga aag aag gct gtg cct gtt gag tct cct gtg cag aag gtt 1414
 Gln Arg Gly Lys Lys Ala Val Pro Val Glu Ser Pro Val Gln Lys Val

420

425

430

tgagggtgga aagggcctga ggggtgaagt gaaataggac cctcccacca tccccttctg 1474

ctgtaacctc tgaggagct ggctgaaagg gcaaaatgca ggtgttttct cagtatcaca 1534

gaccagctct gcagcagggg attggggagc ccaggaggca gccttccctt ttgccttaag 1594

tcacccatct tccagtaagc agtttattct gagccccggg ggtagacagt cctcagtgag 1654

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aagtccctt aagcttggc ctagctgtgc tctgccacct tccagactca cteccctctg 1774

caaatacctg catttcttac cctggtgaga aaagcacaag cgggtgtaggc tccaatgctg 1834

cttcccagg aggggtgaaga tgggtctgtg ctgaggaaag gggatgcaga gccctgcca 1894

gcaccaccac ctctatgct cctggatccc taggctctgt tccatgagcc tgttgcaggt 1954

tttggtaatt tagaaatgta actttttgct cttataattt tattttatta aattaaatta 2014

ctgc 2018

<210> 87

<211> 235

<212> PRT

<213> Homo sapiens

<400> 87

Met Gly Ile Gly Lys Ser Lys Ile Asn Ser Cys Pro Leu Ser Leu Ser

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15

Trp Gly Lys Arg His Ser Val Asp Thr Ser Pro Gly Tyr His Glu Ser

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25

30

Asp Ser Lys Lys Ser Glu Asp Leu Ser Leu Cys Asn Val Ala Glu His

35

40

45

Ser Asn Thr Thr Glu Gly Pro Thr Gly Lys Gln Glu Gly Ala Gln Ser

50

55

60

Val Glu Glu Met Phe Glu Glu Glu Ala Glu Glu Glu Val Phe Leu Lys

65

70

75

80

Phe Val Ile Leu His Ala Glu Asp Asp Thr Asp Glu Ala Leu Arg Val

85

90

95

Gln Asn Leu Leu Gln Asp Asp Phe Gly Ile Lys Pro Gly Ile Ile Phe

100

105

110

Ala Glu Met Pro Cys Gly Arg Gln His Leu Gln Asn Leu Asp Asp Ala

115

120

125

Val Asn Gly Ser Ala Trp Thr Ile Leu Leu Leu Thr Glu Asn Phe Leu

130

135

140

Arg Asp Thr Trp Cys Asn Phe Gln Phe Tyr Thr Ser Leu Met Asn Ser

145

150

155

160

Val Asn Arg Gln His Lys Tyr Asn Ser Val Ile Pro Met Arg Pro Leu

165

170

175

Asn Asn Pro Leu Pro Arg Glu Arg Thr Pro Phe Ala Leu Gln Thr Ile

180

185

190

Asn Ala Leu Glu Glu Glu Ser Arg Gly Phe Pro Thr Gln Val Glu Arg

195

200

205

Ile Phe Gln Glu Ser Val Tyr Lys Thr Gln Gln Thr Ile Trp Lys Glu

210

215

220

Thr Arg Asn Met Val Gln Arg Gln Phe Ile Ala

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<210> 88

<211> 2717

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (111).. (815)

<400> 88

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aaatgctgag aaatacataa agttttcctc ttctgccttg gatatttata atg ggt 116

Met Gly

1

atc ggg aag tct aaa ata aat tcc tgc cct ctt tct ctc tct tgg ggt 164

Ile Gly Lys Ser Lys Ile Asn Ser Cys Pro Leu Ser Leu Ser Trp Gly
 5 10 15

aaa agg cac agt gtg gat aca agt cca gga tat cat gag tca gat tcc 212
 Lys Arg His Ser Val Asp Thr Ser Pro Gly Tyr His Glu Ser Asp Ser
 20 25 30

aag aag tct gaa gat cta tcc ttg tgt aat gtt gct gag cac agc aat 260
 Lys Lys Ser Glu Asp Leu Ser Leu Cys Asn Val Ala Glu His Ser Asn
 35 40 45 50

aca aca gag ggg cca aca gga aag cag gag gga gct cag agc gtg gaa 308
 Thr Thr Glu Gly Pro Thr Gly Lys Gln Glu Gly Ala Gln Ser Val Glu
 55 60 65

gag atg ttt gaa gaa gaa gct gaa gaa gag gtg ttc ctc aaa ttt gtg 356
 Glu Met Phe Glu Glu Glu Ala Glu Glu Glu Val Phe Leu Lys Phe Val
 70 75 80

ata ttg cat gca gaa gat gac aca gat gaa gcc ctc aga gtc cag aat 404
 Ile Leu His Ala Glu Asp Asp Thr Asp Glu Ala Leu Arg Val Gln Asn
 85 90 95

ctg cta caa gat gac ttt ggt atc aaa ccc gga ata atc ttt gct gag 452
 Leu Leu Gln Asp Asp Phe Gly Ile Lys Pro Gly Ile Ile Phe Ala Glu
 100 105 110

atg cca tgt ggc aga cag cat tta cag aat tta gat gat gct gta aat 500
 Met Pro Cys Gly Arg Gln His Leu Gln Asn Leu Asp Asp Ala Val Asn

115	120	125	130	
ggg tct gca tgg aca atc tta tta ctg act gaa aac ttt tta aga gat				548
Gly Ser Ala Trp Thr Ile Leu Leu Leu Thr Glu Asn Phe Leu Arg Asp				
	135	140	145	
act tgg tgt aat ttc cag ttc tat acg tcc cta atg aac tcc gtt aac				596
Thr Trp Cys Asn Phe Gln Phe Tyr Thr Ser Leu Met Asn Ser Val Asn				
	150	155	160	
agg cag cat aaa tac aac tct gtt ata ccc atg cgg ccc ctg aac aat				644
Arg Gln His Lys Tyr Asn Ser Val Ile Pro Met Arg Pro Leu Asn Asn				
	165	170	175	
ccc ctt ccc cga gaa agg act ccc ttt gcc ctc caa acc atc aat gcc				692
Pro Leu Pro Arg Glu Arg Thr Pro Phe Ala Leu Gln Thr Ile Asn Ala				
	180	185	190	
tta gag gaa gaa agt cgt gga ttt cct aca caa gta gaa aga att ttt				740
Leu Glu Glu Glu Ser Arg Gly Phe Pro Thr Gln Val Glu Arg Ile Phe				
	195	200	205	210
cag gag tct gtg tat aag aca caa caa act ata tgg aaa gag aca aga				788
Gln Glu Ser Val Tyr Lys Thr Gln Gln Thr Ile Trp Lys Glu Thr Arg				
	215	220	225	
aat atg gta caa aga caa ttt att gcc tgagatgaaa catataacat				835
Asn Met Val Gln Arg Gln Phe Ile Ala				
	230	235		

gtggctggct cttgttttgt aaaccaaag attaatcttc acttgagaaa gcagtttcta 895

ggaaatgttt aaataaaaga gagtcttcac cttaaagaaa cctatggagc acaagaaaga 955

taaatttctg caggacagcc tataaaattg tggtagtttt tgatgtttca gtaaacttga 1015

cattgtcaga gtticaagga cttttcttcc acaattttcc tagttcatgg ataigaaaaa 1075

ggaattctca atccatattc ctgtattga accttgaaca aaaacttgta tgacagacat 1135

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cttctaaaag gcgtataact gtgtgagtg ccagatattc actttttaga tcaaaaacct 1615

ctcttatgga agctttaaaa gtttccgtca cacacaattc tcttctcagg aagtatttct 1675

catitaggtc ttcaaagtag cctgactgtg tgcattgtgtg tgtgtgatag gttatttata 1735

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tgagattgag ggagcatcgt ccacttgaga tcagggatgg ggtggagaat gggtcattgtc 1915

atgtaatgag aaaagccctc ttccgggatca tgagacttgg ttctagtcca atttctgcc 1975

ctgaggatga atgtaactgt gggcaaacta ttacctctcc ttatctgtg aaatgaaagg 2035

gttgaattga tggatctcta aaggcttttg tctctatga ggatgtgaaa aactagggac 2095

cacaaaaggg aacaagcaaa aaagtttggg ttcgataaag tgatatgtaa tagttgcaga 2155

aggctttata tatgcttata atgaaaagat attttttga tattgacagc ataatttatt 2215

tttaatgctg tcattacact taaagtcaca ggaaaaaaat atacatgctt actcaggctt 2275

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agtattcatt tttttgccat aatgcttctt gtaaagccaa ttttatatac taataaaaca 2635

tgaactgccc actcttcatg cctgccaaac ttggggcaat tgatgctaaa tggatatttt 2695

aaaataaatg tttttattct tt

2717

<210> 89

<211> 245

<212> PRT

<213> Homo sapiens

<400> 89

Met Ala Ser Pro Ser Arg Arg Leu Gln Thr Lys Pro Val Ile Thr Cys

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Phe Lys Ser Val Leu Leu Ile Tyr Thr Phe Ile Phe Trp Ile Thr Gly

20

25

30

Val Ile Leu Leu Ala Val Gly Ile Trp Gly Lys Val Ser Leu Glu Asn

35

40

45

Tyr Phe Ser Leu Leu Asn Glu Lys Ala Thr Asn Val Pro Phe Val Leu

50

55

60

Ile Ala Thr Gly Thr Val Ile Ile Leu Leu Gly Thr Phe Gly Cys Phe

65

70

75

80

Ala Thr Cys Arg Ala Ser Ala Trp Met Leu Lys Leu Tyr Ala Met Phe
85 90 95

Leu Thr Leu Val Phe Leu Val Glu Leu Val Ala Ala Ile Val Gly Phe
100 105 110

Val Phe Arg His Glu Ile Lys Asn Ser Phe Lys Asn Asn Tyr Glu Lys
115 120 125

Ala Leu Lys Gln Tyr Asn Ser Thr Gly Asp Tyr Arg Ser His Ala Val
130 135 140

Asp Lys Ile Gln Asn Thr Leu His Cys Cys Gly Val Thr Asp Tyr Arg
145 150 155 160

Asp Trp Thr Asp Thr Asn Tyr Tyr Ser Glu Lys Gly Phe Pro Lys Ser
165 170 175

Cys Cys Lys Leu Glu Asp Cys Thr Pro Gln Arg Asp Ala Asp Lys Val
180 185 190

Asn Asn Glu Gly Cys Phe Ile Lys Val Met Thr Ile Ile Glu Ser Glu
195 200 205

Met Gly Val Val Ala Gly Ile Ser Phe Gly Val Ala Cys Phe Gln Leu
210 215 220

Ile Gly Ile Phe Leu Ala Tyr Cys Leu Ser Arg Ala Ile Thr Asn Asn
225 230 235 240

Gln Tyr Glu Ile Val

245

<210> 90

<211> 1793

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (60).. (794)

<400> 90

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atg gcg tcc ccg tct cgg aga ctg cag act aaa cca gtc att act tgt 107

Met Ala Ser Pro Ser Arg Arg Leu Gln Thr Lys Pro Val Ile Thr Cys

1

5

10

15

ttc aag agc gtt ctg cta atc tac act ttt att ttc tgg atc act ggc 155

Phe Lys Ser Val Leu Leu Ile Tyr Thr Phe Ile Phe Trp Ile Thr Gly

20

25

30

gtt atc ctt ctt gca gtt ggc att tgg ggc aag gtg agc ctg gag aat 203

Val Ile Leu Leu Ala Val Gly Ile Trp Gly Lys Val Ser Leu Glu Asn

35

40

45

tac ttt tct ctt tta aat gag aag gcc acc aat gtc ccc ttc gtg ctc 251
Tyr Phe Ser Leu Leu Asn Glu Lys Ala Thr Asn Val Pro Phe Val Leu

50

55

60

att gct act ggt acc gtc att att ctt ttg ggc acc ttt ggt tgt ttt 299
Ile Ala Thr Gly Thr Val Ile Ile Leu Leu Gly Thr Phe Gly Cys Phe

65

70

75

80

gct acc tgc cga gct tct gca tgg atg cta aaa ctg tat gca atg ttt 347
Ala Thr Cys Arg Ala Ser Ala Trp Met Leu Lys Leu Tyr Ala Met Phe

85

90

95

ctg act ctc gtt ttt ttg gtc gaa ctg gtc gct gcc atc gta gga ttt 395
Leu Thr Leu Val Phe Leu Val Glu Leu Val Ala Ala Ile Val Gly Phe

100

105

110

gtt ttc aga cat gag att aag aac agc ttt aag aat aat tat gag aag 443
Val Phe Arg His Glu Ile Lys Asn Ser Phe Lys Asn Asn Tyr Glu Lys

115

120

125

gct ttg aag cag tat aac tct aca gga gat tat aga agc cat gca gta 491
Ala Leu Lys Gln Tyr Asn Ser Thr Gly Asp Tyr Arg Ser His Ala Val

130

135

140

gac aag atc caa aat acg ttg cat tgt tgt ggt gtc acc gat tat aga 539
Asp Lys Ile Gln Asn Thr Leu His Cys Cys Gly Val Thr Asp Tyr Arg

145

150

155

160

gat tgg aca gat act aat tat tac tca gaa aaa gga ttt cct aag agt 587

Asp Trp Thr Asp Thr Asn Tyr Tyr Ser Glu Lys Gly Phe Pro Lys Ser
 165 170 175

tgc tgt aaa ctt gaa gat tgt act cca cag aga gat gca gac aaa gta 635
 Cys Cys Lys Leu Glu Asp Cys Thr Pro Gln Arg Asp Ala Asp Lys Val
 180 185 190

aac aat gaa ggt tgt ttt ata aag gtg atg acc att ata gag tca gaa 683
 Asn Asn Glu Gly Cys Phe Ile Lys Val Met Thr Ile Ile Glu Ser Glu
 195 200 205

atg gga gtc gtt gca gga att tcc ttt gga gtt gct tgc ttc caa ctg 731
 Met Gly Val Val Ala Gly Ile Ser Phe Gly Val Ala Cys Phe Gln Leu
 210 215 220

att gga atc ttt ctc gcc tac tgc ctc tct cgt gcc ata aca aat aac 779
 Ile Gly Ile Phe Leu Ala Tyr Cys Leu Ser Arg Ala Ile Thr Asn Asn
 225 230 235 240

cag tat gag ata gtg taacccaatg tatctgtggg cctattcctc tctacctta 834
 Gln Tyr Glu Ile Val
 245

aggacattta gggcccccc tgtgaattag aaagttgctt ggctggagaa ctgacaacac 894

tacttactga tagaccaaaa aactacacca gtaggttgat tcaatcaaga tgtatgtaga 954

cctaaaacta caccaatagg ctgattcaat caagatccgt gctcgcagtg ggctgattca 1014

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<210> 91

<211> 180

<212> PRT

<213> Homo sapiens

<400> 91

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Asp Lys Arg Cys Lys Leu Leu Leu Gly Ile Gly Ile Leu Val Leu Leu

20 25 30

Ile Ile Val Ile Leu Gly Val Pro Leu Ile Ile Phe Thr Ile Lys Ala

35 40 45

Asn Ser Glu Ala Cys Arg Asp Gly Leu Arg Ala Val Met Glu Cys Arg

50 55 60

Asn Val Thr His Leu Leu Gln Gln Glu Leu Thr Glu Ala Gln Lys Gly

65 70 75 80

Phe Gln Asp Val Glu Ala Gln Ala Ala Thr Cys Asn His Thr Val Met

85 90 95

Ala Leu Met Ala Ser Leu Asp Ala Glu Lys Ala Gln Gly Gln Lys Lys

100 105 110

Val Glu Glu Leu Glu Gly Glu Ile Thr Thr Leu Asn His Lys Leu Gln

115 120 125

Asp Ala Ser Ala Glu Val Glu Arg Leu Arg Arg Glu Asn Gln Val Leu

130

135

140

Ser Val Arg Ile Ala Asp Lys Lys Tyr Tyr Pro Ser Ser Gln Asp Ser

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150

155

160

Ser Ser Ala Ala Ala Pro Gln Leu Leu Ile Val Leu Leu Gly Leu Ser

165

170

175

Ala Leu Leu Gln

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<210> 92

<211> 970

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (26).. (565)

<400> 92

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Met Ala Ser Thr Ser Tyr Asp Tyr Cys

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aga gtg ccc atg gaa gac ggg gat aag cgc tgt aag ctt ctg ctg ggg 100

Arg Val Pro Met Glu Asp Gly Asp Lys Arg Cys Lys Leu Leu Leu Gly

10

15

20

25

ata gga att ctg gtg ctc ctg atc atc gtg att ctg ggg gtg ccc ttg 148

Ile Gly Ile Leu Val Leu Leu Ile Ile Val Ile Leu Gly Val Pro Leu

30

35

40

att atc ttc acc atc aag gcc aac agc gag gcc tgc cgg gac ggc ctt 196

Ile Ile Phe Thr Ile Lys Ala Asn Ser Glu Ala Cys Arg Asp Gly Leu

45

50

55

cgg gca gtg atg gag tgt cgc aat gtc acc cat ctc ctg caa caa gag 244

Arg Ala Val Met Glu Cys Arg Asn Val Thr His Leu Leu Gln Gln Glu

60

65

70

ctg acc gag gcc cag aag ggc ttt cag gat gtg gag gcc cag gct gcc 292

Leu Thr Glu Ala Gln Lys Gly Phe Gln Asp Val Glu Ala Gln Ala Ala

75

80

85

acc tgc aac cac act gtg atg gcc cta atg gct tcc ctg gat gca gag 340

Thr Cys Asn His Thr Val Met Ala Leu Met Ala Ser Leu Asp Ala Glu

90

95

100

105

aag gcc caa gga caa aag aaa gtg gag gag ctt gag gga gag atc act 388

Lys Ala Gln Gly Gln Lys Lys Val Glu Glu Leu Glu Gly Glu Ile Thr

110

115

120

aca tta aac cat aag ctt cag gac gcg tct gca gag gtg gag cga ctg 436

Thr Leu Asn His Lys Leu Gln Asp Ala Ser Ala Glu Val Glu Arg Leu

125

130

135

aga aga gaa aac cag gtc tta agc gtg aga atc gcg gac aag aag tac 484
Arg Arg Glu Asn Gln Val Leu Ser Val Arg Ile Ala Asp Lys Lys Tyr

140

145

150

tac ccc agc tcc cag gac tcc agc tcc gct gcg gcg ccc cag ctg ctg 532
Tyr Pro Ser Ser Gln Asp Ser Ser Ser Ala Ala Ala Pro Gln Leu Leu

155

160

165

att gtg ctg ctg ggc ctc agc gct ctg ctg cag tgagatccca ggaagctggc 585
Ile Val Leu Leu Gly Leu Ser Ala Leu Leu Gln

170

175

180

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gcctctggag caggtctgga ggggccatgg ggcagtcctg ggtgtgggga cacagtcggg 765

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cttcctttga gggagagcac acctt 970

<210> 93

<211> 331

<212> PRT

<213> Homo sapiens

<400> 93

Met Asp Ser Glu Lys Lys Arg Phe Thr Glu Glu Ala Thr Lys Tyr Phe

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Arg Glu Arg Val Ser Pro Val His Leu Gln Ile Leu Leu Thr Asn Asn

20

25

30

Glu Ala Trp Lys Arg Phe Val Thr Ala Ala Glu Leu Pro Arg Asp Glu

35

40

45

Ala Asp Ala Leu Tyr Glu Ala Leu Lys Lys Leu Arg Thr Tyr Ala Ala

50

55

60

Ile Glu Asp Glu Tyr Val Gln Gln Lys Asp Glu Gln Phe Arg Glu Trp

65

70

75

80

Phe Leu Lys Glu Phe Pro Gln Val Lys Arg Lys Ile Gln Glu Ser Ile

85

90

95

Glu Lys Leu Arg Ala Leu Ala Asn Gly Ile Glu Glu Val His Arg Gly

100

105

110

Cys Thr Ile Ser Asn Val Val Ser Ser Ser Thr Gly Ala Ala Ser Gly

115

120

125

Ile Met Ser Leu Ala Gly Leu Val Leu Ala Pro Phe Thr Ala Gly Thr

130

135

140

Ser Leu Ala Leu Thr Ala Ala Gly Val Gly Leu Gly Ala Ala Ser Ala

145

150

155

160

Val Thr Gly Ile Thr Thr Ser Ile Val Glu His Ser Tyr Thr Ser Ser

165

170

175

Ala Glu Ala Glu Ala Ser Arg Leu Thr Ala Thr Ser Ile Asp Arg Leu

180

185

190

Lys Val Phe Lys Glu Val Met Arg Asp Ile Thr Pro Asn Leu Leu Ser

195

200

205

Leu Leu Asn Asn Tyr Tyr Glu Ala Thr Gln Thr Ile Gly Ser Glu Ile

210

215

220

Arg Ala Ile Arg Gln Ala Arg Ala Arg Ala Arg Leu Pro Val Thr Thr

225

230

235

240

Trp Arg Ile Ser Ala Gly Ser Gly Gly Gln Ala Glu Arg Thr Ile Ala

245

250

255

Gly Thr Thr Arg Ala Val Ser Arg Gly Ala Arg Ile Leu Ser Ala Thr

260

265

270

Thr Ser Gly Ile Phe Leu Ala Leu Asp Val Val Asn Leu Val Tyr Glu

275

280

285

Ser Lys His Leu His Glu Gly Ala Lys Ser Ala Ser Ala Glu Glu Leu
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Arg Arg Gln Ala Gln Glu Leu Glu Glu Asn Leu Met Glu Leu Thr Gln
 305 310 315 320

Ile Tyr Gln Arg Leu Asn Pro Cys His Thr His
 325 330

<210> 94

<211> 2039

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (175).. (1167)

<400> 94

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tcagtgcactg gagagctcca aggaaagtct ctacgtgacc tggctgctgg cacc atg 177

Met

1

gac tca gaa aag aaa cgc ttt act gaa gag gcc acc aaa tac ttc cgg 225

Asp Ser Glu Lys Lys Arg Phe Thr Glu Glu Ala Thr Lys Tyr Phe Arg

5

10

15

gag aga gtc agc cca gtg cat ctg caa atc ctg ctg act aac aat gaa 273

Glu Arg Val Ser Pro Val His Leu Gln Ile Leu Leu Thr Asn Asn Glu

20

25

30

gcc tgg aag aga ttc gtg act gcg gct gaa ttg ccc agg gat gag gca 321

Ala Trp Lys Arg Phe Val Thr Ala Ala Glu Leu Pro Arg Asp Glu Ala

35

40

45

gat gct ctc tac gaa gct ctg aag aag ctt aga aca tat gca gct att 369

Asp Ala Leu Tyr Glu Ala Leu Lys Lys Leu Arg Thr Tyr Ala Ala Ile

50

55

60

65

gag gac gaa tat gtg cag cag aaa gat gag cag ttt agg gaa tgg ttt 417

Glu Asp Glu Tyr Val Gln Gln Lys Asp Glu Gln Phe Arg Glu Trp Phe

70

75

80

ttg aaa gag ttt ccc caa gtc aag agg aag atc cag gag tcc ata gaa 465

Leu Lys Glu Phe Pro Gln Val Lys Arg Lys Ile Gln Glu Ser Ile Glu

85

90

95

aag ctt cgt gcc ctt gca aat ggt att gaa gag gtc cac aga ggc tgc 513

Lys Leu Arg Ala Leu Ala Asn Gly Ile Glu Glu Val His Arg Gly Cys

100

105

110

acc atc tcc aac gtg gtg tcc agc tcc act ggc gct gcc tct ggc atc 561

Thr Ile Ser Asn Val Val Ser Ser Ser Thr Gly Ala Ala Ser Gly Ile

115	120	125	
atg tcc ctt gct ggt ctt gtt ttg gca cca ttt aca gca ggg acg agt 609			
Met Ser Leu Ala Gly Leu Val Leu Ala Pro Phe Thr Ala Gly Thr Ser			
130	135	140	145
ctg gcc ctt act gca gct ggg gta ggg ctg gga gca gcg tct gct gtg 657			
Leu Ala Leu Thr Ala Ala Gly Val Gly Leu Gly Ala Ala Ser Ala Val			
150	155	160	
act ggg atc acc acc agc atc gtg gag cac tca tac aca tca tca gca 705			
Thr Gly Ile Thr Thr Ser Ile Val Glu His Ser Tyr Thr Ser Ser Ala			
165	170	175	
gaa gct gaa gcc agc agg ctg act gca acc agc att gac cga ttg aag 753			
Glu Ala Glu Ala Ser Arg Leu Thr Ala Thr Ser Ile Asp Arg Leu Lys			
180	185	190	
gta ttt aag gaa gtt atg cgt gac atc aca ccc aac tta ctt tcc ctt 801			
Val Phe Lys Glu Val Met Arg Asp Ile Thr Pro Asn Leu Leu Ser Leu			
195	200	205	
ctt aat aat tat tac gaa gcc aca caa acc att ggg agt gaa atc cgt 849			
Leu Asn Asn Tyr Tyr Glu Ala Thr Gln Thr Ile Gly Ser Glu Ile Arg			
210	215	220	225
gcc atc agg caa gcc aga gcc agg gcc cga ctc cct gtg acc acc tgg 897			
Ala Ile Arg Gln Ala Arg Ala Arg Ala Arg Leu Pro Val Thr Thr Trp			
230	235	240	

cga atc tca gct gga agt ggt ggt caa gca gag aga acg att gca ggc 945

Arg Ile Ser Ala Gly Ser Gly Gly Gln Ala Glu Arg Thr Ile Ala Gly

245

250

255

acc acc cgg gca gtg agc aga gga gcc cgg atc ctg agt gcg acc act 993

Thr Thr Arg Ala Val Ser Arg Gly Ala Arg Ile Leu Ser Ala Thr Thr

260

265

270

tca ggc atc ttc ctt gca ctg gat gtg gtc aac ctt gta tac gag tca 1041

Ser Gly Ile Phe Leu Ala Leu Asp Val Val Asn Leu Val Tyr Glu Ser

275

280

285

aag cac ttg cat gag ggg gca aag tct gca tct gct gag gag ctg agg 1089

Lys His Leu His Glu Gly Ala Lys Ser Ala Ser Ala Glu Glu Leu Arg

290

295

300

305

cgg cag gct cag gag ctg gag gag aat cta atg gag ctc act cag atc 1137

Arg Gln Ala Gln Glu Leu Glu Glu Asn Leu Met Glu Leu Thr Gln Ile

310

315

320

tat cag cgt ctg aat cca tgc cat acc cac tgaccccgaga ccagtcgagc 1187

Tyr Gln Arg Leu Asn Pro Cys His Thr His

325

330

cagcagggga ggtgagccat acacaggcca cgacaaaatg caggcatittt attaggggga 1247

taaagagggc aaggtaaagt ttatggagct gactgttagt gactttggca tttctgtagc 1307

tgagcacagc aggggagggg ttaatgcaga tggcaagtgc accaaggaga aggcaggaat 1367
gctggagcct ggaataaggg aggagagggg actggagagt gtggggaata ggaagaagaa 1427
atttccttta gactaacgaa tataattggg ggaggaatag aggggaggig tgcaggaacc 1487
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tctctaaaaa cccaacatc ctggagagta tgcgagaacc taccaagaaa aacagtctca 1907
ttactcatat acagcaggca aagagacaga aaattaactg aaaagcagtt tagagactgg 1967
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cacctactca cc 2039

<210> 95

<211> 407

<212> PRT

<213> Homo sapiens

<400> 95

Met Glu Leu Leu Glu Glu Asp Leu Thr Cys Pro Ile Cys Cys Ser Leu

1 5 10 15

Phe Asp Asp Pro Arg Val Leu Pro Cys Ser His Asn Phe Cys Lys Lys

20 25 30

Cys Leu Glu Gly Ile Leu Glu Gly Ser Val Arg Asn Ser Leu Trp Arg

35 40 45

Pro Ala Pro Phe Lys Cys Pro Thr Cys Arg Lys Glu Thr Ser Ala Thr

50 55 60

Gly Ile Asn Ser Leu Gln Val Asn Tyr Ser Leu Lys Gly Ile Val Glu

65 70 75 80

Lys Tyr Asn Lys Ile Lys Ile Ser Pro Lys Met Pro Val Cys Lys Gly

85 90 95

His Leu Gly Gln Pro Leu Asn Ile Phe Cys Leu Thr Asp Met Gln Leu

100 105 110

Ile Cys Gly Ile Cys Ala Thr Arg Gly Glu His Thr Lys His Val Phe

115 120 125

Cys Ser Ile Glu Asp Ala Tyr Ala Gln Glu Arg Asp Ala Phe Glu Ser

130	135	140	
Leu Phe Gln Ser Phe Glu Thr Trp Arg Arg Gly Asp Ala Leu Ser Arg			
145	150	155	160
Leu Asp Thr Leu Glu Thr Ser Lys Arg Lys Ser Leu Gln Leu Leu Thr			
165	170	175	
Lys Asp Ser Asp Lys Val Lys Glu Phe Phe Glu Lys Leu Gln His Thr			
180	185	190	
Leu Asp Gln Lys Lys Asn Glu Ile Leu Ser Asp Phe Glu Thr Met Lys			
195	200	205	
Leu Ala Val Met Gln Ala Tyr Asp Pro Glu Ile Asn Lys Leu Asn Thr			
210	215	220	
Ile Leu Gln Glu Gln Arg Met Ala Phe Asn Ile Ala Glu Ala Phe Lys			
225	230	235	240
Asp Val Ser Glu Pro Ile Val Phe Leu Gln Gln Met Gln Glu Phe Arg			
245	250	255	
Glu Lys Ile Lys Val Ile Lys Glu Thr Pro Leu Pro Pro Ser Asn Leu			
260	265	270	
Pro Ala Ser Pro Leu Met Lys Asn Phe Asp Thr Ser Gln Trp Glu Asp			
275	280	285	

Ile Lys Leu Val Asp Val Asp Lys Leu Ser Leu Pro Gln Asp Thr Gly
290 295 300

Thr Phe Ile Ser Lys Ile Pro Trp Ser Phe Tyr Lys Leu Phe Leu Leu
305 310 315 320

Ile Leu Leu Leu Gly Leu Val Ile Val Phe Gly Pro Thr Met Phe Leu
325 330 335

Glu Trp Ser Leu Phe Asp Asp Leu Ala Thr Trp Lys Gly Cys Leu Ser
340 345 350

Asn Phe Ser Ser Tyr Leu Thr Lys Thr Ala Asp Phe Ile Glu Gln Ser
355 360 365

Val Phe Tyr Trp Glu Gln Val Thr Asp Gly Phe Phe Ile Phe Asn Glu
370 375 380

Arg Phe Lys Asn Phe Thr Leu Val Val Leu Asn Asn Val Ala Glu Phe
385 390 395 400

Val Cys Lys Tyr Lys Leu Leu
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<210> 96

<211> 1409

<212> DNA

<213> Homo sapiens

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<222> (181).. (1401)

<400> 96

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tttgccctgg gaaatagtaa ccctgccaaa tacatcagct tgtaggagac agaggatgtg 180

atg gag ctg ctt gaa gaa gat ctc aca tgc cct att tgt tgt agt ctg 228

Met Glu Leu Leu Glu Glu Asp Leu Thr Cys Pro Ile Cys Cys Ser Leu

1

5

10

15

ttt gat gat cca cgg gtt ttg cct tgc tcc cac aac ttc tgc aaa aaa 276

Phe Asp Asp Pro Arg Val Leu Pro Cys Ser His Asn Phe Cys Lys Lys

20

25

30

tgc tta gaa ggt atc tta gaa ggg agt gtg cgg aat tcc ttg tgg aga 324

Cys Leu Glu Gly Ile Leu Glu Gly Ser Val Arg Asn Ser Leu Trp Arg

35

40

45

cca gct cca ttc aag tgt cct aca tgc cgt aag gaa act tca gct act 372

Pro Ala Pro Phe Lys Cys Pro Thr Cys Arg Lys Glu Thr Ser Ala Thr

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55

60

gga att aat agc ctg cag gtt aat tac tcc ctg aag ggt att gtg gaa 420

Gly Ile Asn Ser Leu Gln Val Asn Tyr Ser Leu Lys Gly Ile Val Glu

65 70 75 80

aag tat aac aag atc aag atc tct ccc aaa atg cca gta tgc aaa gga 468

Lys Tyr Asn Lys Ile Lys Ile Ser Pro Lys Met Pro Val Cys Lys Gly

85 90 95

cac ttg ggg cag cct ctc aac att ttc tgc ctg act gat atg cag ctg 516

His Leu Gly Gln Pro Leu Asn Ile Phe Cys Leu Thr Asp Met Gln Leu

100 105 110

att tgt ggg atc tgt gct act cgt ggg gag cac acc aaa cat gtc ttc 564

Ile Cys Gly Ile Cys Ala Thr Arg Gly Glu His Thr Lys His Val Phe

115 120 125

tgt tct att gaa gat gcc tat gct cag gaa agg gat gcc ttt gag tcc 612

Cys Ser Ile Glu Asp Ala Tyr Ala Gln Glu Arg Asp Ala Phe Glu Ser

130 135 140

ctc ttc cag agc ttt gag acc tgg cgt cgg gga gat gct ctt tct cgc 660

Leu Phe Gln Ser Phe Glu Thr Trp Arg Arg Gly Asp Ala Leu Ser Arg

145 150 155 160

ttg gat acc ttg gaa act agt aag agg aaa tcc cta cag tta ctg act 708

Leu Asp Thr Leu Glu Thr Ser Lys Arg Lys Ser Leu Gln Leu Leu Thr

165 170 175

aaa gat tca gat aaa gtg aag gaa ttt ttt gag aag tta caa cac aca 756

Lys Asp Ser Asp Lys Val Lys Glu Phe Phe Glu Lys Leu Gln His Thr

180

185

190

ctg gat caa aag aag aat gaa att ctg tct gac ttt gag acc atg aaa 804

Leu Asp Gln Lys Lys Asn Glu Ile Leu Ser Asp Phe Glu Thr Met Lys

195

200

205

ctt gct gtt atg caa gca tat gac cca gag atc aac aaa ctc aac acc 852

Leu Ala Val Met Gln Ala Tyr Asp Pro Glu Ile Asn Lys Leu Asn Thr

210

215

220

atc ttg cag gag caa cgg atg gcc ttt aac att gct gag gct ttc aaa 900

Ile Leu Gln Glu Gln Arg Met Ala Phe Asn Ile Ala Glu Ala Phe Lys

225

230

235

240

gat gtg tca gaa ccc att gta ttt ctg caa cag atg cag gag ttt aga 948

Asp Val Ser Glu Pro Ile Val Phe Leu Gln Gln Met Gln Glu Phe Arg

245

250

255

gag aaa atc aaa gta atc aag gaa act cct tta cct ccc tct aat ttg 996

Glu Lys Ile Lys Val Ile Lys Glu Thr Pro Leu Pro Pro Ser Asn Leu

260

265

270

cct gca agc cct tta atg aag aac ttt gat acc agt cag tgg gaa gac 1044

Pro Ala Ser Pro Leu Met Lys Asn Phe Asp Thr Ser Gln Trp Glu Asp

275

280

285

ata aaa cta gtc gat gtg gat aaa ctt tct ttg cct caa gac act ggc 1092

Ile Lys Leu Val Asp Val Asp Lys Leu Ser Leu Pro Gln Asp Thr Gly

290

295

300

aca ttc att agc aag att ccc tgg agc ttt tat aag tta ttt ttg cta 1140

Thr Phe Ile Ser Lys Ile Pro Trp Ser Phe Tyr Lys Leu Phe Leu Leu

305

310

315

320

atc ctt ctg ctt ggc ctt gtc att gtc ttt ggt cct acc atg ttc cta 1188

Ile Leu Leu Leu Gly Leu Val Ile Val Phe Gly Pro Thr Met Phe Leu

325

330

335

gaa tgg tca tta ttt gat gac ctg gca act tgg aaa ggc tgt ctt tca 1236

Glu Trp Ser Leu Phe Asp Asp Leu Ala Thr Trp Lys Gly Cys Leu Ser

340

345

350

aac ttc agt tcc tat ctg act aaa aca gcc gat ttc ata gaa caa tca 1284

Asn Phe Ser Ser Tyr Leu Thr Lys Thr Ala Asp Phe Ile Glu Gln Ser

355

360

365

gtt ttt tac tgg gaa cag gtg aca gat ggg ttt ttc att ttc aat gaa 1332

Val Phe Tyr Trp Glu Gln Val Thr Asp Gly Phe Phe Ile Phe Asn Glu

370

375

380

aga ttc aag aat ttt act ttg gtg gta ctg aac aat gtg gca gaa ttt 1380

Arg Phe Lys Asn Phe Thr Leu Val Val Leu Asn Asn Val Ala Glu Phe

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395

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gtg tgc aaa tat aaa cta tta taaaatcg

1409

Val Cys Lys Tyr Lys Leu Leu

405

<210> 97

<211> 465

<212> PRT

<213> Homo sapiens

<400> 97

Met Ala Ser Thr Thr Ser Thr Lys Lys Met Met Glu Glu Ala Thr Cys

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Ser Ile Cys Leu Ser Leu Met Thr Asn Pro Val Ser Ile Asn Cys Gly

20

25

30

His Ser Tyr Cys His Leu Cys Ile Thr Asp Phe Phe Lys Asn Pro Ser

35

40

45

Gln Lys Gln Leu Arg Gln Glu Thr Phe Cys Cys Pro Gln Cys Arg Ala

50

55

60

Pro Phe His Met Asp Ser Leu Arg Pro Asn Lys Gln Leu Gly Ser Leu

65

70

75

80

Ile Glu Ala Leu Lys Glu Thr Asp Gln Glu Met Ser Cys Glu Glu His

85

90

95

Gly Glu Gln Phe His Leu Phe Cys Glu Asp Glu Gly Gln Leu Ile Cys

100

105

110

Trp Arg Cys Glu Arg Ala Pro Gln His Lys Gly His Thr Thr Ala Leu

115

120

125

Val Glu Asp Val Cys Gln Gly Tyr Lys Glu Lys Leu Gln Glu Ala Val

130

135

140

Thr Lys Leu Lys Gln Leu Glu Asp Arg Cys Thr Glu Gln Lys Leu Ser

145

150

155

160

Thr Ala Met Arg Ile Thr Lys Trp Lys Glu Lys Val Gln Ile Gln Arg

165

170

175

Gln Lys Ile Arg Ser Asp Phe Lys Asn Leu Gln Cys Phe Leu His Glu

180

185

190

Glu Glu Lys Ser Tyr Leu Trp Arg Leu Glu Lys Glu Glu Gln Gln Thr

195

200

205

Leu Ser Arg Leu Arg Asp Tyr Glu Ala Gly Leu Gly Leu Lys Ser Asn

210

215

220

Glu Leu Lys Ser His Ile Leu Glu Leu Glu Glu Lys Cys Gln Gly Ser

225

230

235

240

Ala Gln Lys Leu Leu Gln Asn Val Asn Asp Thr Leu Ser Arg Ser Trp

245

250

255

Ala Val Lys Leu Glu Thr Ser Glu Ala Val Ser Leu Glu Leu His Thr

260

265

270

Met Cys Asn Val Ser Lys Leu Tyr Phe Asp Val Lys Lys Met Leu Arg
275 280 285

Ser His Gln Val Ser Val Thr Leu Asp Pro Asp Thr Ala His His Glu
290 295 300

Leu Ile Leu Ser Glu Asp Arg Arg Gln Val Thr Arg Gly Tyr Thr Gln
305 310 315 320

Glu Asn Gln Asp Thr Ser Ser Arg Arg Phe Thr Ala Phe Pro Cys Val
325 330 335

Leu Gly Cys Glu Gly Phe Thr Ser Gly Arg Arg Tyr Phe Glu Val Asp
340 345 350

Val Gly Glu Gly Thr Gly Trp Asp Leu Gly Val Cys Met Glu Asn Val
355 360 365

Gln Arg Gly Thr Gly Met Lys Gln Glu Pro Gln Ser Gly Phe Trp Thr
370 375 380

Leu Arg Leu Cys Lys Lys Lys Gly Tyr Val Ala Leu Thr Ser Pro Pro
385 390 395 400

Thr Ser Leu His Leu His Glu Gln Pro Leu Leu Val Gly Ile Phe Leu
405 410 415

Asp Tyr Glu Ala Gly Val Val Ser Phe Tyr Asn Gly Asn Thr Gly Cys
420 425 430

His Ile Phe Thr Phe Pro Lys Ala Ser Phe Ser Asp Thr Leu Arg Pro

435

440

445

Tyr Phe Gln Val Tyr Gln Tyr Ser Pro Leu Phe Leu Pro Pro Pro Gly

450

455

460

Asp

465

<210> 98

<211> 1940

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (477).. (1871)

<400> 98

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ccttgggaagg aggggagccc catctcccca gaagagcagt gaccccagca gagagggggc 180

tggtgtatca ctggaggaaa tagcctgcc aggaatacac gtcttcagaa gaagttctgt 240

gtggcttcaa gagactgac aaattgtgag aggaaaacag cctacccggt cctcttttct 300

tcaatacaaa atgagataat aggggttga aggaaaacct tcaagaccta tggaagtcag 360

ttgcagccag ctcacacat agaggtgcag gtgagggtga ttttcacac ggtggaaaat 420

tctggctgct tcctccat cctagagcc aatattggag cttttcaata aaagct atg 479

Met

1

gcc tca acc acc agc acc aag aag atg atg gag gaa gcc acc tgc tcc 527

Ala Ser Thr Thr Ser Thr Lys Lys Met Met Glu Glu Ala Thr Cys Ser

5

10

15

atc tgc ctg agc ctg atg acg aac cca gta agc atc aac tgt gga cac 575

Ile Cys Leu Ser Leu Met Thr Asn Pro Val Ser Ile Asn Cys Gly His

20

25

30

agc tac tgc cac ttg tgt ata aca gac ttc ttt aaa aac cca agc caa 623

Ser Tyr Cys His Leu Cys Ile Thr Asp Phe Phe Lys Asn Pro Ser Gln

35

40

45

aag caa ctg agg cag gag aca ttc tgc tgt ccc cag tgt cgg gct cca 671

Lys Gln Leu Arg Gln Glu Thr Phe Cys Cys Pro Gln Cys Arg Ala Pro

50

55

60

65

ttt cat atg gat agc ctc cga ccc aac aag cag ctg gga agc ctc att 719

Phe His Met Asp Ser Leu Arg Pro Asn Lys Gln Leu Gly Ser Leu Ile

70

75

80

gaa gcc ctc aaa gag acg gat caa gaa atg tca tgt gag gaa cac gga 767

Glu Ala Leu Lys Glu Thr Asp Gln Glu Met Ser Cys Glu Glu His Gly

85

90

95

gag cag ttc cac ctg ttc tgc gaa gac gag ggg cag ctc atc tgc tgg 815

Glu Gln Phe His Leu Phe Cys Glu Asp Glu Gly Gln Leu Ile Cys Trp

100

105

110

cgc tgt gag cgg gca cca cag cac aaa ggg cac acc aca gct ctt gtt 863

Arg Cys Glu Arg Ala Pro Gln His Lys Gly His Thr Thr Ala Leu Val

115

120

125

gaa gac gta tgc cag ggc tac aag gaa aag ctc cag gaa gct gtg aca 911

Glu Asp Val Cys Gln Gly Tyr Lys Glu Lys Leu Gln Glu Ala Val Thr

130

135

140

145

aaa ctg aag caa ctt gaa gac aga tgt acg gag cag aag ctg tcc aca 959

Lys Leu Lys Gln Leu Glu Asp Arg Cys Thr Glu Gln Lys Leu Ser Thr

150

155

160

gca atg cga ata act aaa tgg aaa gag aag gta cag att cag aga caa 1007

Ala Met. Arg Ile Thr Lys Trp Lys Glu Lys Val Gln Ile Gln Arg Gln

165

170

175

aaa atc cgg tct gac ttt aag aat ctc cag tgt ttc cta cat gag gaa 1055

Lys Ile Arg Ser Asp Phe Lys Asn Leu Gln Cys Phe Leu His Glu Glu

180

185

190

gag aag tct tat ctc tgg agg ctg gag aaa gaa gaa caa cag act ctg 1103
 Glu Lys Ser Tyr Leu Trp Arg Leu Glu Lys Glu Glu Gln Gln Thr Leu
 195 200 205

agt aga ctg agg gac tat gag gct ggt ctg ggg ctg aag agc aat gaa 1151
 Ser Arg Leu Arg Asp Tyr Glu Ala Gly Leu Gly Leu Lys Ser Asn Glu
 210 215 220 225

ctc aag agc cac atc ctg gaa ctg gag gaa aaa tgt cag ggc tca gcc 1199
 Leu Lys Ser His Ile Leu Glu Leu Glu Glu Lys Cys Gln Gly Ser Ala
 230 235 240

cag aaa ttg ctg cag aat gtg aat gac act ttg agc agg agt tgg gct 1247
 Gln Lys Leu Leu Gln Asn Val Asn Asp Thr Leu Ser Arg Ser Trp Ala
 245 250 255

gtg aag ctg gaa aca tca gag gct gtc tcc ttg gaa ctt cat act atg 1295
 Val Lys Leu Glu Thr Ser Glu Ala Val Ser Leu Glu Leu His Thr Met
 260 265 270

tgc aat gtt tcc aag ctt tac ttc gat gtg aag aaa atg tta agg agt 1343
 Cys Asn Val Ser Lys Leu Tyr Phe Asp Val Lys Lys Met Leu Arg Ser
 275 280 285

cat caa gtt agt gtg act ctg gat cca gat aca gct cat cac gaa cta 1391
 His Gln Val Ser Val Thr Leu Asp Pro Asp Thr Ala His His Glu Leu
 290 295 300 305

att ctc tct gag gat cgg aga caa gtg act cgt gga tac acc cag gag 1439

Ile Leu Ser Glu Asp Arg Arg Gln Val Thr Arg Gly Tyr Thr Gln Glu
 310 315 320

aat cag gac aca tct tcc agg aga ttt act gcc ttc ccc tgt gtc ttg 1487
 Asn Gln Asp Thr Ser Ser Arg Arg Phe Thr Ala Phe Pro Cys Val Leu
 325 330 335

ggt tgt gaa ggc ttc acc tca gga aga cgt tac ttt gaa gtg gat gtt 1535
 Gly Cys Glu Gly Phe Thr Ser Gly Arg Arg Tyr Phe Glu Val Asp Val
 340 345 350

ggc gaa gga acc gga tgg gat tta gga gtt tgt atg gaa aat gtg cag 1583
 Gly Glu Gly Thr Gly Trp Asp Leu Gly Val Cys Met Glu Asn Val Gln
 355 360 365

agg ggc act ggc atg aag caa gag cct cag tct gga ttc tgg acc ctc 1631
 Arg Gly Thr Gly Met Lys Gln Glu Pro Gln Ser Gly Phe Trp Thr Leu
 370 375 380 385

agg ctg tgc aaa aag aaa ggc tat gta gca ctt act tct ccc cca act 1679
 Arg Leu Cys Lys Lys Lys Gly Tyr Val Ala Leu Thr Ser Pro Pro Thr
 390 395 400

tcc ctt cat ctg cat gag cag ccc ctg ctt gtg gga att ttt ctg gac 1727
 Ser Leu His Leu His Glu Gln Pro Leu Leu Val Gly Ile Phe Leu Asp
 405 410 415

tat gag gcc gga gtt gta tcc ttt tat aac ggg aat act ggc tgc cac 1775
 Tyr Glu Ala Gly Val Val Ser Phe Tyr Asn Gly Asn Thr Gly Cys His

420

425

430

atc ttt act ttc ccg aag gct tcc ttc tct gat act ctc cgg ccc tat 1823

Ile Phe Thr Phe Pro Lys Ala Ser Phe Ser Asp Thr Leu Arg Pro Tyr

435

440

445

ttc cag gtt tat caa tat tct cct ttg ttt ctg cct ccc cca ggt gac 1871

Phe Gln Val Tyr Gln Tyr Ser Pro Leu Phe Leu Pro Pro Pro Gly Asp

450

455

460

465

taaggaaaag agcagaagct ccttggttta accagcacag agaaaataat ataaatccca 1931

taagggcag

1940

<210> 99

<211> 465

<212> PRT

<213> Homo sapiens

<400> 99

Met Ala Ser Thr Thr Ser Thr Lys Lys Met Met Glu Glu Ala Thr Cys

1

5

10

15

Ser Ile Cys Leu Ser Leu Met Thr Asn Pro Val Ser Ile Asn Cys Gly

20

25

30

His Ser Tyr Cys His Leu Cys Ile Thr Asp Phe Phe Lys Asn Pro Ser

35

40

45

Gln Lys Gln Leu Arg Gln Glu Thr Phe Cys Cys Pro Gln Cys Arg Ala
50 55 60

Pro Phe His Met Asp Ser Leu Arg Pro Asn Lys Gln Leu Gly Ser Leu
65 70 75 80

Ile Glu Ala Leu Lys Glu Thr Asp Gln Glu Met Ser Cys Glu Glu His
85 90 95

Gly Glu Gln Phe His Leu Phe Cys Glu Asp Glu Gly Gln Leu Ile Cys
100 105 110

Trp Arg Cys Glu Arg Ala Pro Gln His Lys Gly His Thr Thr Ala Leu
115 120 125

Val Glu Asp Val Cys Gln Gly Tyr Lys Glu Lys Leu Gln Lys Ala Val
130 135 140

Thr Lys Leu Lys Gln Leu Glu Asp Arg Cys Thr Glu Gln Lys Leu Ser
145 150 155 160

Thr Ala Met Arg Ile Thr Lys Trp Lys Glu Lys Val Gln Ile Gln Arg
165 170 175

Gln Lys Ile Arg Ser Asp Phe Lys Asn Leu Gln Cys Phe Leu His Glu
180 185 190

Glu Glu Lys Ser Tyr Leu Trp Arg Leu Glu Lys Glu Glu Gln Gln Thr

195

200

205

Leu Ser Arg Leu Arg Asp Tyr Glu Ala Gly Leu Gly Leu Lys Ser Asn

210

215

220

Glu Leu Lys Ser His Ile Leu Glu Leu Glu Glu Lys Cys Gln Gly Ser

225

230

235

240

Ala Gln Lys Leu Leu Gln Asn Val Asn Asp Thr Leu Ser Arg Ser Trp

245

250

255

Ala Val Lys Leu Glu Thr Ser Glu Ala Val Ser Leu Glu Leu His Thr

260

265

270

Met Cys Asn Val Ser Lys Leu Tyr Phe Asp Val Lys Lys Met Leu Arg

275

280

285

Ser His Gln Val Ser Val Thr Leu Asp Pro Asp Thr Ala His His Glu

290

295

300

Leu Ile Leu Ser Glu Asp Arg Arg Gln Val Thr Arg Gly Tyr Thr Gln

305

310

315

320

Glu Asn Gln Asp Thr Ser Ser Arg Arg Phe Thr Ala Phe Pro Cys Val

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Leu Gly Cys Glu Gly Phe Thr Ser Gly Arg Arg Tyr Phe Glu Val Asp

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Val Gly Glu Gly Thr Gly Trp Asp Leu Gly Val Cys Met Glu Asn Val
355 360 365

Gln Arg Gly Thr Gly Met Lys Gln Glu Pro Gln Ser Gly Phe Trp Thr
370 375 380

Leu Arg Leu Cys Lys Lys Lys Gly Tyr Val Ala Leu Thr Ser Pro Pro
385 390 395 400

Thr Ser Leu His Leu His Glu Gln Pro Leu Leu Val Gly Ile Phe Leu
405 410 415

Asp Tyr Glu Ala Gly Val Val Ser Phe Tyr Asn Gly Asn Thr Gly Cys
420 425 430

His Ile Phe Thr Phe Pro Lys Ala Ser Phe Ser Asp Thr Leu Arg Pro
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Tyr Phe Gln Val Tyr Gln Tyr Ser Pro Leu Phe Leu Pro Pro Pro Gly
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ccttgggaagg aggggagccc catctcccca gaagagcagt gacccagca gagaggggcc 180

tggtgtatca ctggaggaaa tagcctgcc aggaatacac gtcttcagaa gaagtctgt 240

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tcaatacaaa atgagataat aggggttggg aggaaaacct tcaagacctg tggaagtcag 360

ttgcagccag ctcatcacat agaggctgcag gtgagggtga tttcatcac ggtggaaaat 420

tctggctgct tcctctccat ctctagagcc aatatggag cttttcaata aaagct atg 479

Met

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gcc tca acc acc agc acc aag aag atg atg gag gaa gcc acc tgc tcc 527

Ala Ser Thr Thr Ser Thr Lys Lys Met Met Glu Glu Ala Thr Cys Ser

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atc tgc ctg agc ctg atg acg aac cca gta agc atc aac tgt gga cac 575

Ile Cys Leu Ser Leu Met Thr Asn Pro Val Ser Ile Asn Cys Gly His

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agc tac tgc cac ttg tgt ata aca gac ttc ttt aaa aac cca agc caa 623

Ser Tyr Cys His Leu Cys Ile Thr Asp Phe Phe Lys Asn Pro Ser Gln

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aag caa ctg agg cag gag aca ttc tgc tgt ccc cag tgt cgg gct cca 671

Lys Gln Leu Arg Gln Glu Thr Phe Cys Cys Pro Gln Cys Arg Ala Pro

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ttt cat atg gat agc ctc cga ccc aac aag cag ctg gga agc ctc att 719

Phe His Met Asp Ser Leu Arg Pro Asn Lys Gln Leu Gly Ser Leu Ile

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gaa gcc ctc aaa gag acg gat caa gaa atg tca tgt gag gaa cac gga 767

Glu Ala Leu Lys Glu Thr Asp Gln Glu Met Ser Cys Glu Glu His Gly

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gag cag ttc cac ctg ttc tgc gaa gac gag ggg cag ctc atc tgc tgg 815

Glu Gln Phe His Leu Phe Cys Glu Asp Glu Gly Gln Leu Ile Cys Trp

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cgc tgt gag cgg gca cca cag cac aaa ggg cac acc aca gct ctt gtt 863

Arg Cys Glu Arg Ala Pro Gln His Lys Gly His Thr Thr Ala Leu Val

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Glu Asp Val Cys Gln Gly Tyr Lys Glu Lys Leu Gln Lys Ala Val Thr

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Lys Leu Lys Gln Leu Glu Asp Arg Cys Thr Glu Gln Lys Leu Ser Thr				
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gca atg cga ata act aaa tgg aaa gag aag gta cag att cag aga caa				1007
Ala Met Arg Ile Thr Lys Trp Lys Glu Lys Val Gln Ile Gln Arg Gln				
	165	170	175	
aaa atc cgg tct gac ttt aag aat ctc cag tgt ttc cta cat gag gaa				1055
Lys Ile Arg Ser Asp Phe Lys Asn Leu Gln Cys Phe Leu His Glu Glu				
	180	185	190	
gag aag tct tat ctc tgg agg ctg gag aaa gaa gaa caa cag act ctg				1103
Glu Lys Ser Tyr Leu Trp Arg Leu Glu Lys Glu Glu Gln Gln Thr Leu				
	195	200	205	
agt aga ctg agg gac tat gag gct ggt ctg ggg ctg aag agc aat gaa				1151
Ser Arg Leu Arg Asp Tyr Glu Ala Gly Leu Gly Leu Lys Ser Asn Glu				
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ctc aag agc cac atc ctg gaa ctg gag gaa aaa tgt cag ggc tca gcc				1199
Leu Lys Ser His Ile Leu Glu Leu Glu Glu Lys Cys Gln Gly Ser Ala				
	230	235	240	
cag aaa ttg ctg cag aat gtg aat gac act ttg agc agg agt tgg gct				1247
Gln Lys Leu Leu Gln Asn Val Asn Asp Thr Leu Ser Arg Ser Trp Ala				
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gtg aag ctg gaa aca tca gag gct gtc tcc ttg gaa ctt cat act atg 1295

Val Lys Leu Glu Thr Ser Glu Ala Val Ser Leu Glu Leu His Thr Met

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tgc aat gtt tcc aag ctt tac ttc gat gtg aag aaa atg tta agg agt 1343

Cys Asn Val Ser Lys Leu Tyr Phe Asp Val Lys Lys Met Leu Arg Ser

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cat caa gtt agt gtg act ctg gat cca gat aca gct cat cac gaa cta 1391

His Gln Val Ser Val Thr Leu Asp Pro Asp Thr Ala His His Glu Leu

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att ctc tct gag gat cgg aga caa gtg act cgt gga tac acc cag gag 1439

Ile Leu Ser Glu Asp Arg Arg Gln Val Thr Arg Gly Tyr Thr Gln Glu

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ggc gaa gga acc gga tgg gat tta gga gtt tgt atg gaa aat gtg cag 1535

Gly Cys Glu Gly Phe Thr Ser Gly Arg Arg Tyr Phe Glu Val Asp Val

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ggc gaa gga acc gga tgg gat tta gga gtt tgt atg gaa aat gtg cag 1583

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agg ggc act ggc atg aag caa gag cct cag tct gga ttc tgg acc ctc 1631
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agg ctg tgc aaa aag aaa ggc tat gta gca ctt act tct ccc cca act 1679
 Arg Leu Cys Lys Lys Lys Gly Tyr Val Ala Leu Thr Ser Pro Pro Thr
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tcc ctt cat ctg cat gag cag ccc ctg ctt gtg gga att ttt ctg-gac 1727
 Ser Leu His Leu His Glu Gln Pro Leu Leu Val Gly Ile Phe Leu Asp
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tat gag gcc gga gtt gta tcc ttt tat aac ggg aat act ggc tgc cac 1775
 Tyr Glu Ala Gly Val Val Ser Phe Tyr Asn Gly Asn Thr Gly Cys His
 420 425 430

atc ttt act ttc ccg aag gct tcc ttc tct gat act ctc cgg ccc tat 1823
 Ile Phe Thr Phe Pro Lys Ala Ser Phe Ser Asp Thr Leu Arg Pro Tyr
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ttc cag gtt tat caa tat tct cct ttg ttt ctg cct ccc cca ggt gac 1871
 Phe Gln Val Tyr Gln Tyr Ser Pro Leu Phe Leu Pro Pro Pro Gly Asp
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taagggcag

1940

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Lys Arg Pro Pro Gln Pro Pro Glu Glu Ser Gln Pro Pro Gln Ser Gln

35 40 45

Ala Gln Val Pro Pro Ala Ala Pro His His His His His Ser His

50 55 60

Ser Gly Pro Glu Ile Ser Arg Ile Ile Val Asp Pro Thr Thr Gly Lys

65 70 75 80

Arg Tyr Cys Arg Gly Lys Val Leu Gly Lys Gly Gly Phe Ala Lys Cys

85 90 95

Tyr Glu Met Thr Asp Leu Thr Asn Asn Lys Val Tyr Ala Ala Lys Ile

100 105 110

Ile Pro His Ser Arg Val Ala Lys Pro His Gln Arg Glu Lys Ile Asp

115 120 125

Lys Glu Ile Glu Leu His Arg Ile Leu His His Lys His Val Val Gln
130 135 140

Phe Tyr His Tyr Phe Glu Asp Lys Glu Asn Ile Tyr Ile Leu Leu Glu
145 150 155 160

Tyr Cys Ser Arg Arg Ser Met Ala His Ile Leu Lys Ala Arg Lys Val
165 170 175

Leu Thr Glu Pro Glu Val Arg Tyr Tyr Leu Arg Gln Ile Val Ser Gly
180 185 190

Leu Lys Tyr Leu His Glu Gln Glu Ile Leu His Arg Asp Leu Lys Leu
195 200 205

Gly Asn Phe Phe Ile Asn Glu Ala Met Glu Leu Lys Val Gly Asp Phe
210 215 220

Gly Leu Ala Ala Arg Leu Glu Pro Leu Glu His Arg Arg Arg Thr Ile
225 230 235 240

Cys Gly Thr Pro Asn Tyr Leu Ser Pro Glu Val Leu Asn Lys Gln Gly
245 250 255

His Gly Cys Glu Ser Asp Ile Trp Ala Leu Gly Cys Val Met Tyr Thr
260 265 270

Met Leu Leu Gly Arg Pro Pro Phe Glu Thr Thr Asn Leu Lys Glu Thr

275

280

285

Tyr Arg Cys Ile Arg Glu Ala Arg Tyr Thr Met Pro Ser Ser Leu Leu

290

295

300

Ala Pro Ala Lys His Leu Ile Ala Ser Met Leu Ser Lys Asn Pro Glu

305

310

315

320

Asp Arg Pro Ser Leu Asp Asp Ile Ile Arg His Asp Phe Phe Leu Gln

325

330

335

Gly Phe Thr Pro Asp Arg Leu Ser Ser Ser Cys Cys His Thr Val Pro

340

345

350

Asp Phe His Leu Ser Ser Pro Ala Lys Asn Phe Phe Lys Lys Ala Ala

355

360

365

Ala Ala Leu Phe Gly Gly Lys Lys Asp Lys Ala Arg Tyr Ile Asp Thr

370

375

380

His Asn Arg Val Ser Lys Glu Asp Glu Asp Ile Tyr Lys Leu Arg His

385

390

395

400

Asp Leu Lys Lys Thr Ser Ile Thr Gln Gln Pro Ser Lys His Arg Thr

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410

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Asp Glu Glu Leu Gln Pro Pro Thr Thr Thr Val Ala Arg Ser Gly Thr

420

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Pro Ala Val Glu Asn Lys Gln Gln Ile Gly Asp Ala Ile Arg Met Ile
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Val Arg Gly Thr Leu Gly Ser Cys Ser Ser Ser Ser Glu Cys Leu Glu
450 455 460

Asp Ser Thr Met Gly Ser Val Ala Asp Thr Val Ala Arg Val Leu Arg
465 470 475 480

Gly Cys Leu Glu Asn Met Pro Glu Ala Asp Cys Ile Pro Lys Glu Gln
485 490 495

Leu Ser Thr Ser Phe Gln Trp Val Thr Lys Trp Val Asp Tyr Ser Asn
500 505 510

Lys Tyr Gly Phe Gly Tyr Gln Leu Ser Asp His Thr Val Gly Val Leu
515 520 525

Phe Asn Asn Gly Ala His Met Ser Leu Leu Pro Asp Lys Lys Thr Val
530 535 540

His Tyr Tyr Ala Glu Leu Gly Gln Cys Ser Val Phe Pro Ala Thr Asp
545 550 555 560

Ala Pro Glu Gln Phe Ile Ser Gln Val Thr Val Leu Lys Tyr Phe Ser
565 570 575

His Tyr Met Glu Glu Asn Leu Met Asp Gly Gly Asp Leu Pro Ser Val
580 585 590

Thr Asp Ile Arg Arg Pro Arg Leu Tyr Leu Leu Gln Trp Leu Lys Ser
595 600 605

Asp Lys Ala Leu Met Met Leu Phe Asn Asp Gly Thr Phe Gln Val Asn
610 615 620

Phe Tyr His Asp His Thr Lys Ile Ile Ile Cys Ser Gln Asn Glu Glu
625 630 635 640

Tyr Leu Leu Thr Tyr Ile Asn Glu Asp Arg Ile Ser Thr Thr Phe Arg
645 650 655

Leu Thr Thr Leu Leu Met Ser Gly Cys Ser Ser Glu Leu Lys Asn Arg
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ggcgacc atg gag ctt ttg cgg act atc acc tac cag cca gcc gcc agc 169

Met Glu Leu Leu Arg Thr Ile Thr Tyr Gln Pro Ala Ala Ser

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acc aaa atg tgc gag cag gcg ctg ggc aag ggt tgc gga gca gac tcg 217

Thr Lys Met Cys Glu Gln Ala Leu Gly Lys Gly Cys Gly Ala Asp Ser

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25

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aag aag aag cgg ccg ccg cag ccc ccc gag gaa tcg cag cca cct cag 265

Lys Lys Lys Arg Pro Pro Gln Pro Pro Glu Glu Ser Gln Pro Pro Gln

35

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tcc cag gcg caa gtg ccc ccg gcg gcc cct cac cac cat cac cac cat 313

Ser Gln Ala Gln Val Pro Pro Ala Ala Pro His His His His His His

50

55

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tcg cac tcg ggg ccg gag atc tcg cgg att atc gtc gac ccc acg act 361

Ser His Ser Gly Pro Glu Ile Ser Arg Ile Ile Val Asp Pro Thr Thr

65

70

75

ggg aag cgc tac tgc cgg ggc aaa gtg ctg gga aag ggt ggc ttt gca 409

Gly Lys Arg Tyr Cys Arg Gly Lys Val Leu Gly Lys Gly Gly Phe Ala

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85

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aaa tgt tac gag atg aca gat ttg aca aat aac aaa gtc tac gcc gca 457

Lys Cys Tyr Glu Met Thr Asp Leu Thr Asn Asn Lys Val Tyr Ala Ala

95 100 105 110

aaa att att cct cac agc aga gta gct aaa cct cat caa agg gaa aag 505

Lys Ile Ile Pro His Ser Arg Val Ala Lys Pro His Gln Arg Glu Lys

115 120 125

att gac aaa gaa ata gag ctt cac aga att ctt cat cat aag cat gta 553

Ile Asp Lys Glu Ile Glu Leu His Arg Ile Leu His His Lys His Val

130 135 140

gtg cag ttt tac cac tac ttc gag gac aaa gaa aac att tac att ctc 601

Val Gln Phe Tyr His Tyr Phe Glu Asp Lys Glu Asn Ile Tyr Ile Leu

145 150 155

ttg gaa tac tgc agt aga agg tca atg gct cat att ttg aaa gca aga 649

Leu Glu Tyr Cys Ser Arg Arg Ser Met Ala His Ile Leu Lys Ala Arg

160 165 170

aag gtg ttg aca gag cca gaa gtt cga tac tac ctc agg cag att gtg 697

Lys Val Leu Thr Glu Pro Glu Val Arg Tyr Tyr Leu Arg Gln Ile Val

175 180 185 190

tct gga ctg aaa tac ctt cat gaa caa gaa atc ttg cac aga gat ctc 745

Ser Gly Leu Lys Tyr Leu His Glu Gln Glu Ile Leu His Arg Asp Leu

195 200 205

aaa cta ggg aac ttt ttt att aat gaa gcc atg gaa cta aaa gtt ggg 793

Lys Leu Gly Asn Phe Phe Ile Asn Glu Ala Met Glu Leu Lys Val Gly

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215

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gac ttc ggt ctg gca gcc agg cta gaa ccc ttg gaa cac aga agg aga 841

Asp Phe Gly Leu Ala Ala Arg Leu Glu Pro Leu Glu His Arg Arg Arg

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acg ata tgt ggt acc cca aat tat ctc tct cct gaa gtc ctc aac aaa 889

Thr Ile Cys Gly Thr Pro Asn Tyr Leu Ser Pro Glu Val Leu Asn Lys

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caa gga cat ggc tgt gaa tca gac att tgg gcc ctg ggc tgt gta atg 937

Gln Gly His Gly Cys Glu Ser Asp Ile Trp Ala Leu Gly Cys Val Met

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tat aca atg tta cta ggg agg ccc cca ttt gaa act aca aat ctc aaa 985

Tyr Thr Met Leu Leu Gly Arg Pro Pro Phe Glu Thr Thr Asn Leu Lys

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gaa act tat agg tgc ata agg gaa gca agg tat aca atg ccg tcc tca 1033

Glu Thr Tyr Arg Cys Ile Arg Glu Ala Arg Tyr Thr Met Pro Ser Ser

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ttg ctg gct cct gcc aag cac tta att gct agt atg ttg tcc aaa aac 1081

Leu Leu Ala Pro Ala Lys His Leu Ile Ala Ser Met Leu Ser Lys Asn

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cca gag gat cgt ccc agt ttg gat gac atc att cga cat gac ttt ttt 1129

Pro Glu Asp Arg Pro Ser Leu Asp Asp Ile Ile Arg His Asp Phe Phe

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gtt cca gat ttc cac tta tca agc cca gct aag aat ttc ttt aag aaa			1225
Val Pro Asp Phe His Leu Ser Ser Pro Ala Lys Asn Phe Phe Lys Lys			
355	360	365	
gca gct gct gct ctt ttt ggt ggc aaa aaa gac aaa gca aga tat att			1273
Ala Ala Ala Ala Leu Phe Gly Gly Lys Lys Asp Lys Ala Arg Tyr Ile			
370	375	380	
gac aca cat aat aga gtg tct aaa gaa gat gaa gac atc tac aag ctt			1321
Asp Thr His Asn Arg Val Ser Lys Glu Asp Glu Asp Ile Tyr Lys Leu			
385	390	395	
agg cat gat ttg aaa aag act tca ata act cag caa ccc agc aaa cac			1369
Arg His Asp Leu Lys Lys Thr Ser Ile Thr Gln Gln Pro Ser Lys His			
400	405	410	
agg aca gat gag gag ctc cag cca cct acc acc aca gtt gcc agg tct			1417
Arg Thr Asp Glu Glu Leu Gln Pro Pro Thr Thr Thr Val Ala Arg Ser			
415	420	425	430
gga aca ccc gca gta gaa aac aag cag cag att ggg gat gct att cgg			1465
Gly Thr Pro Ala Val Glu Asn Lys Gln Gln Ile Gly Asp Ala Ile Arg			
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ctt gaa gac agt acc atg gga agt gtt gca gac aca gtg gca agg gtt 1561
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470

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ctt cgg gga tgt ctg gaa aac atg ccg gaa gct gat tgc att ccc aaa 1609
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490

gag cag ctg agc aca tca ttt cag tgg gtc acc aaa tgg gtt gat tac 1657
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495 500 505 510

tct aac aaa tat ggc ttt ggg tac cag ctc tca gac cac acc gtc ggt 1705
Ser Asn Lys Tyr Gly Phe Gly Tyr Gln Leu Ser Asp His Thr Val Gly

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gtc ctt ttc aac aat ggt gct cac atg agc ctc ctt cca gac aaa aaa 1753
Val Leu Phe Asn Asn Gly Ala His Met Ser Leu Leu Pro Asp Lys Lys

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540

aca gtt cac tat tac gca gag ctt ggc caa tgc tca gtt ttc cca gca 1801
Thr Val His Tyr Tyr Ala Glu Leu Gly Gln Cys Ser Val Phe Pro Ala

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aca gat gct cct gag caa ttt att agt caa gtg acg gtg ctg aaa tac 1849
 Thr Asp Ala Pro Glu Gln Phe Ile Ser Gln Val Thr Val Leu Lys Tyr
 560 565 570

ttt tct cat tac atg gag gag aac ctc atg gat ggt gga gat ctg cct 1897
 Phe Ser His Tyr Met Glu Glu Asn Leu Met Asp Gly Gly Asp Leu Pro
 575 580 585 590

agt gtt act gat att cga aga cct cgg ctc tac ctc ctt cag tgg cta 1945
 Ser Val Thr Asp Ile Arg Arg Pro Arg Leu Tyr Leu Leu Gln Trp Leu
 595 600 605

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 Lys Ser Asp Lys Ala Leu Met Met Leu Phe Asn Asp Gly Thr Phe Gln
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 Val Asn Phe Tyr His Asp His Thr Lys Ile Ile Ile Cys Ser Gln Asn
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 Glu Glu Tyr Leu Leu Thr Tyr Ile Asn Glu Asp Arg Ile Ser Thr Thr
 640 645 650

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 Phe Arg Leu Thr Thr Leu Leu Met Ser Gly Cys Ser Ser Glu Leu Lys
 655 660 665 670

aat cga atg gaa tat gcc ctg aac atg ctc tta caa aga tgt aac 2182

Asn Arg Met Glu Tyr Ala Leu Asn Met Leu Leu Gln Arg Cys Asn

675

680

685

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2783

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<213> Homo sapiens

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Tyr Pro Thr Pro Pro Ala Pro Met Pro Gly Pro Thr Thr Gly Leu Val

35 40 45

Thr Gly Pro Asp Gly Lys Gly Met Asn Pro Pro Ser Tyr Tyr Thr Gln

50 55 60

Pro Ala Pro Ile Pro Asn Asn Asn Pro Ile Thr Val Gln Thr Val Tyr

65 70 75 80

Val Gln His Pro Ile Thr Phe Leu Asp Arg Pro Ile Gln Met Cys Cys

85 90 95

Pro Ser Cys Asn Lys Met Ile Val Ser Gln Leu Ser Tyr Asn Ala Gly

100 105 110

Ala Leu Thr Trp Leu Ser Cys Gly Ser Leu Cys Leu Leu Gly Cys Ile

115 120 125

Ala Gly Cys Cys Phe Ile Pro Phe Cys Val Asp Ala Leu Gln Asp Val

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Asp His Tyr Cys Pro Asn Cys Arg Ala Leu Leu Gly Thr Tyr Lys Arg

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Leu

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Met Ser Val Pro Gly Pro Tyr Gln Ala Ala Thr Gly Pro Ser

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tca gca cca tcc gca cct cca tcc tat gaa gag aca gtg gct gtt aac 159

Ser Ala Pro Ser Ala Pro Pro Ser Tyr Glu Glu Thr Val Ala Val Asn

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agt tat tac ccc aca cct cca gct ccc atg cct ggg cca act acg ggg 207

Ser Tyr Tyr Pro Thr Pro Pro Ala Pro Met Pro Gly Pro Thr Thr Gly

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ctt gtg acg ggg cct gat ggg aag ggc atg aat cct cct tgc tat tat 255

Leu Val Thr Gly Pro Asp Gly Lys Gly Met Asn Pro Pro Ser Tyr Tyr

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acc cag cca gcg ccc atc ccc aat aac aat cca att acc gtg cag acg 303

Thr Gln Pro Ala Pro Ile Pro Asn Asn Asn Pro Ile Thr Val Gln Thr

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70

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gtc tac gtg cag cac ccc atc acc ttt ttg gac cgc cct atc caa atg 351

Val Tyr Val Gln His Pro Ile Thr Phe Leu Asp Arg Pro Ile Gln Met

80

85

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tgt tgt cct tcc tgc aac aag atg atc gtg agt cag ctg tcc tat aac 399

Cys Cys Pro Ser Cys Asn Lys Met Ile Val Ser Gln Leu Ser Tyr Asn

95

100

105

110

gcc ggt gct ctg acc tgg ctg tcc tgc ggg agc ctg tgc ctg ctg ggg 447

Ala Gly Ala Leu Thr Trp Leu Ser Cys Gly Ser Leu Cys Leu Leu Gly

115

120

125

tgc ata gcg ggc tgc tgc ttc atc ccc ttc tgc gtg gat gcc ctg cag 495

Cys Ile Ala Gly Cys Cys Phe Ile Pro Phe Cys Val Asp Ala Leu Gln

130

135

140

gac gig gac cat tac tgt ccc aac tgc aga gct ctc ctg ggc acc tac 543

Asp Val Asp His Tyr Cys Pro Asn Cys Arg Ala Leu Leu Gly Thr Tyr

145

150

155

aag cgt ttg taggactcag ccagacgtgg agggagccgg gtgccgcagg 592

Lys Arg Leu

160

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acctctccag ggggccacc ttcattgtctt cttttggggg gaatacgtcg caaaactaac 712

aaatctccaa accccagaaa ttgctgcttg gagtcgtgca taggacttgc aaagacattc 772

cccttgagtg tcagttccac ggtttcctgc ctccctgaga ccttgagtcc tgccatctaa 832

ctgtgatcat tgccctatcc gaatatcttc ctgtgatctg ccatcagtgg ctcttttttc 892

ctgcttccat gggcctttct ggtggcagtc tcaaactgag aagccacagt tgccttattt 952

ttgaggctgt tctgccaga gctcggciga accagcctt agtcctacc attatcttat 1012

ccgtctcttc ccgtccctga tgacaaagat ctgacctac agactttaca ggcttggctt 1072

tgagattctg taactgcaga ctccattagc acacagattc actttaattt ctttaatttt 1132

tttttaaata caaggagggg gctattaaca ccagttacag acatatccac aaggtcgtaa 1192

atgcatgcta gaaaaatagg gctggatctt atcactgcc tgtctccctt tgtttctctg 1252

tgccagatct tcagtcccc ttccataca gggattttt tctcatagag taatttatg 1312

aacagttttt atgacctcct ttgggtctga aatactttcg aacagaattt ctttttttta 1372

aaaaaaaaca gagatggggt cttactatgt tgcccaggct gggtctgaac tcctgggctc 1432

aagcgatcct tctgccttgg cctcccgaag tgcctgggatt gcaggcataa gctaccaatgc 1492

tgggcctgaa cataatttca agaggaggat ttataaaacc attttctgta atcaaattgat 1552

tggtgtcatt ttcccatitg ccaatgtagt ctacatt 1589

<210> 105

<211> 161

<212> PRT

<213> Homo sapiens

<400> 105

Met Ser Val Pro Gly Pro Tyr Gln Ala Ala Thr Gly Pro Ser Ser Ala

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Pro Ser Ala Pro Pro Ser Tyr Glu Glu Thr Val Ala Val Asn Ser Tyr

20 25 30

Tyr Pro Thr Pro Pro Ala Pro Met Pro Gly Pro Thr Thr Gly Leu Val

35 40 45

Thr Gly Pro Asp Gly Lys Gly Met Asn Pro Pro Ser Tyr Tyr Thr Gln

50 55 60

Pro Ala Pro Ile Pro Asn Asn Asn Pro Ile Thr Val Gln Thr Val Tyr
65 70 75 80

Val Gln His Pro Ile Thr Phe Leu Asp Arg Pro Val Gln Met Cys Cys
85 90 95

Pro Ser Cys Asn Lys Met Ile Val Ser Gln Leu Ser Tyr Asn Ala Gly
100 105 110

Ala Leu Thr Trp Leu Ser Cys Gly Ser Leu Cys Leu Leu Gly Cys Ile
115 120 125

Ala Gly Cys Cys Phe Ile Pro Phe Cys Val Asp Ala Leu Gln Asp Val
130 135 140

Asp His Tyr Cys Pro Asn Cys Arg Ala Leu Leu Gly Thr Tyr Lys Arg
145 150 155 160

Leu

<210> 106

<211> 1589

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (70).. (552)

<400> 106

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ggcggtaaa atg tgc gtt cca gga cct tac cag gcg gcc act ggg cct tcc 111

Met Ser Val Pro Gly Pro Tyr Gln Ala Ala Thr Gly Pro Ser

1

5

10

tca gca cca tcc gca cct cca tcc tat gaa gag aca gtg gct gtt aac 159

Ser Ala Pro Ser Ala Pro Pro Ser Tyr Glu Glu Thr Val Ala Val Asn

15

20

25

30

agt tat tac ccc aca cct cca gct ccc atg cct ggg cca act acg ggg 207

Ser Tyr Tyr Pro Thr Pro Pro Ala Pro Met Pro Gly Pro Thr Thr Gly

35

40

45

ctt gtg acg ggg cct gat ggg aag ggc atg aat cct cct tgc tat tat 255

Leu Val Thr Gly Pro Asp Gly Lys Gly Met Asn Pro Pro Ser Tyr Tyr

50

55

60

acc cag cca gcg ccc atc ccc aat aac aat cca att acc gtg cag acg 303

Thr Gln Pro Ala Pro Ile Pro Asn Asn Asn Pro Ile Thr Val Gln Thr

65

70

75

gtc tac gtg cag cac ccc atc acc ttt ttg gac cgc cct gtc caa atg 351

Val Tyr Val Gln His Pro Ile Thr Phe Leu Asp Arg Pro Val Gln Met

80

85

90

tgt tgt cct tcc tgc aac aag atg atc gtg agt cag ctg tcc tat aac 399
 Cys Cys Pro Ser Cys Asn Lys Met Ile Val Ser Gln Leu Ser Tyr Asn
 95 100 105 110

gcc ggt gct ctg acc tgg ctg tcc tgc ggg agc ctg tgc ctg ctg ggg 447
 Ala Gly Ala Leu Thr Trp Leu Ser Cys Gly Ser Leu Cys Leu Leu Gly
 115 120 125

tgc ata gcg ggc tgc tgc ttc atc ccc ttc tgc gtg gat gcc ctg cag 495
 Cys Ile Ala Gly Cys Cys Phe Ile Pro Phe Cys Val Asp Ala Leu Gln
 130 135 140

gac gtg gac cat tac tgt ccc aac tgc aga gct ctc ctg ggc acc tac 543
 Asp Val Asp His Tyr Cys Pro Asn Cys Arg Ala Leu Leu Gly Thr Tyr
 145 150 155

aag cgt ttg taggactcag ccagacgtgg agggagccgg gtgccgcagg 592
 Lys Arg Leu
 160

aagtcctttc cacctctcat ccagcttcac gcctggigga ggttctgccc tggtagtctc 652

acctctccag ggggccacc ttcatgtctt cttttggggg gaatacgtcg caaaactaac 712

aaatctccaa accccagaaa ttgctgcttg gagtcgtgca taggacttgc aaagacattc 772

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ctgtgatcat tgcctatcc gaatacttc ctgtgatctg ccatcagtg ctcttttttc 892

ctgcttccat gggcctttct ggtggcagtc tcaaactgag aagccacagt tgccttattt 952

ttgaggctgt tctgccaga gctcggtga accagcctt agtgccctacc attatcttat 1012

cgtctcttc cgtccctga tgacaaagat ctgacctac agactttaca ggcttggctt 1072

tgagattctg taactgcaga cttcattagc acacagattc actttaattt ctttaatttt 1132

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aacagtttt atgacctctt ttggctga aatactttcg aacagaattt ctttttttta 1372

aaaaaaaaa gagatgggtt ctactatgt tgcccaggct ggtgtcgaac tctgggctc 1432

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tgggcctgaa cataatttca agaggaggat ttataaaacc atttctgta atcaaatgat 1552

tggtgtcatt ttccatttg ccaatgtagt ctactt 1589

<210> 107

<211> 249

<212> PRT

<213> Homo sapiens

<400> 107

Met Ala Ser Ala Ser Gly Ala Met Ala Lys His Glu Gln Ile Leu Val

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Leu Asp Pro Pro Thr Asp Leu Lys Phe Lys Gly Pro Phe Thr Asp Val

20 25 30

Val Thr Thr Asn Leu Lys Leu Arg Asn Pro Ser Asp Arg Lys Val Cys

35 40 45

Phe Lys Val Lys Thr Thr Ala Pro Arg Arg Tyr Cys Val Arg Pro Asn

50 55 60

Ser Gly Ile Ile Asp Pro Gly Ser Thr Val Thr Val Ser Val Met Leu

65 70 75 80

Gln Pro Phe Asp Tyr Asp Pro Asn Glu Lys Ser Lys His Lys Phe Met

85 90 95

Val Gln Thr Ile Phe Ala Pro Pro Asn Thr Ser Asp Met Glu Ala Val

100 105 110

Trp Lys Glu Ala Lys Pro Asp Glu Leu Met Asp Ser Lys Leu Arg Cys

115 120 125

Val Phe Glu Met Pro Asn Glu Asn Asp Lys Leu Asn Asp Met Glu Pro

130

135

140

Ser Lys Ala Val Pro Leu Asn Ala Ser Lys Gln Asp Gly Pro Met Pro

145

150

155

160

Lys Pro His Ser Val Ser Leu Asn Asp Thr Glu Thr Arg Lys Leu Met

165

170

175

Glu Glu Cys Lys Arg Leu Gln Gly Glu Met Met Lys Leu Ser Glu Glu

180

185

190

Asn Arg His Leu Arg Asp Glu Gly Leu Arg Leu Arg Lys Val Ala His

195

200

205

Ser Asp Lys Pro Gly Ser Thr Ser Thr Ala Ser Phe Arg Asp Asn Val

210

215

220

Thr Ser Pro Leu Pro Ser Leu Leu Val Val Ile Ala Ala Ile Phe Ile

225

230

235

240

Gly Phe Phe Leu Gly Lys Phe Ile Leu

245

<210> 108

<211> 1595

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (232).. (978)

<400> 108

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gacccagcgg gtggcccacc gaaccggiga cacagcggca ggcgttaggc ctcgsgagcc 120

gcgagccctgg cctcgtccta gagctcggcc gagccgtcgc cgccgtcgtc ccccgccccc 180

agtcagcaaa ccgccgcgcg gggcgcgccc ccgctctgcg ctgtctctcc g atg gcg 237

Met Ala

1

tcc gcc tca ggg gcc atg gcg aag cac gag cag atc ctg gtc ctc gat 285

Ser Ala Ser Gly Ala Met Ala Lys His Glu Gln Ile Leu Val Leu Asp

5

10

15

ccg ccc aca gac ctc aaa ttc aaa ggc ccc ttc aca gat gta gtc act 333

Pro Pro Thr Asp Leu Lys Phe Lys Gly Pro Phe Thr Asp Val Val Thr

20

25

30

aca aat ctt aaa ttg cga aat cca tcg gat aga aaa gtg tgt ttc aaa 381

Thr Asn Leu Lys Leu Arg Asn Pro Ser Asp Arg Lys Val Cys Phe Lys

35

40

45

50

gtg aag act aca gca cct cgc cgg tac tgt gtg agg ccc aac agt gga 429

Val Lys Thr Thr Ala Pro Arg Arg Tyr Cys Val Arg Pro Asn Ser Gly

55

60

65

att att gac cca ggg tca act gtg act gtt tca gta atg cta cag ccc 477

Ile Ile Asp Pro Gly Ser Thr Val Thr Val Ser Val Met Leu Gln Pro

70

75

80

ttt gac tat gat ccg aat gaa aag agt aaa cac aag ttt atg gta cag 525

Phe Asp Tyr Asp Pro Asn Glu Lys Ser Lys His Lys Phe Met Val Gln

85

90

95

aca att ttt gct cca cca aac act tca gat atg gaa gct gtg tgg aaa 573

Thr Ile Phe Ala Pro Pro Asn Thr Ser Asp Met Glu Ala Val Trp Lys

100

105

110

gag gca aaa cct gat gaa tta atg gat tcc aaa ttg aga tgc gta ttt 621

Glu Ala Lys Pro Asp Glu Leu Met Asp Ser Lys Leu Arg Cys Val Phe

115

120

125

130

gaa atg ccc aat gaa aat gat aaa ttg aat gat atg gaa cct agc aaa 669

Glu Met Pro Asn Glu Asn Asp Lys Leu Asn Asp Met Glu Pro Ser Lys

135

140

145

gct gtt cca ctg aat gca tct aag caa gat gga cct atg cca aaa cca 717

Ala Val Pro Leu Asn Ala Ser Lys Gln Asp Gly Pro Met Pro Lys Pro

150

155

160

cac agt gtt tca ctt aat gat acc gaa aca agg aaa cta atg gaa gag 765

His Ser Val Ser Leu Asn Asp Thr Glu Thr Arg Lys Leu Met Glu Glu

165

170

175

tgt aaa aga ctt cag gga gaa atg atg aag cta tca gaa gaa aat cgg 813

Cys Lys Arg Leu Gln Gly Glu Met Met Lys Leu Ser Glu Glu Asn Arg

180

185

190

cac ctg aga gat gaa ggt tta agg ctc aga aag gta gca cat tcg gat 861

His Leu Arg Asp Glu Gly Leu Arg Leu Arg Lys Val Ala His Ser Asp

195

200

205

210

aaa cct gga tca acc tca act gca tcc ttc aga gat aat gtc acc agt 909

Lys Pro Gly Ser Thr Ser Thr Ala Ser Phe Arg Asp Asn Val Thr Ser

215

220

225

cct ctt cct tca ctt ctt gtt gta att gca gcc att ttc att gga ttc 957

Pro Leu Pro Ser Leu Leu Val Val Ile Ala Ala Ile Phe Ile Gly Phe

230

235

240

ttt cta ggg aaa ttc atc ttg tagagtgaag catgcagagt gctgtttctt 1008

Phe Leu Gly Lys Phe Ile Leu

245

ttttttttt tctcttgacc agaaaaagat ttgtttacct accatttcatt tggtagtatg 1068

gcccacggtg accatttttt tgtgtgtaca gcgtcatata ggctttgcct ttaatgatct 1128

cttacggtta gaaaacacaa taaaaacaaa ctgttcggct actggacagg ttgtatatta 1188

ccagatcatc actagcagat gtcagttgca cattgagtcc tttatgaaat tcataaataa 1248

agaattgttc tttctttgtg gttttaataa gagttcaaga attgttcaga gtcttgtaaa 1308

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atttagattg ctaateccac tcatcagga aatgccaaga ggtattcctt ggggaaatgg 1428

tgccctttac agtgtaaatt tttcctcctt tacctttgct aatatcatgg cagaattttt 1488

cttatccctt gtgaggcagt tgttgactga gtttttcaic cttacaatcc tgtcccatgg 1548

tatttaacat aaaaaaaaaat aaaactgtta acagattcctt gctcgat 1595

<210> 109

<211> 540

<212> PRT

<213> Homo sapiens

<400> 109

Met Gly Thr Thr Ala Arg Ala Ala Leu Val Leu Thr Tyr Leu Ala Val

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Ala Ser Ala Ala Ser Glu Gly Gly Phe Thr Ala Thr Gly Gln Arg Gln

20

25

30

Leu Arg Pro Glu His Phe Gln Glu Val Gly Tyr Ala Ala Pro Pro Ser

35

40

45

Pro Pro Leu Ser Arg Ser Leu Pro Met Asp His Pro Asp Ser Ser Gln

50

55

60

His Gly Pro Pro Phe Glu Gly Gln Ser Gln Val Gln Pro Pro Pro Ser

65

70

75

80

Gln Glu Ala Thr Pro Leu Gln Gln Glu Lys Leu Leu Pro Ala Gln Leu

85

90

95

Pro Ala Glu Lys Glu Val Gly Pro Pro Leu Pro Gln Glu Ala Val Pro

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105

110

Leu Gln Lys Glu Leu Pro Ser Leu Gln His Pro Asn Glu Gln Lys Glu

115

120

125

Gly Thr Pro Ala Pro Phe Gly Asp Gln Ser His Pro Glu Pro Glu Ser

130

135

140

Trp Asn Ala Ala Gln His Cys Gln Gln Asp Arg Ser Gln Gly Gly Trp

145

150

155

160

Gly His Arg Leu Asp Gly Phe Pro Pro Gly Arg Pro Ser Pro Asp Asn

165

170

175

Leu Asn Gln Ile Cys Leu Pro Asn Arg Gln His Val Val Tyr Gly Pro

180

185

190

Trp Asn Leu Pro Gln Ser Ser Tyr Ser His Leu Thr Arg Gln Gly Glu

195

200

205

Thr Leu Asn Phe Leu Glu Ile Gly Tyr Ser Arg Cys Cys His Cys Arg
210 215 220

Ser His Thr Asn Arg Leu Glu Cys Ala Lys Leu Val Trp Glu Glu Ala
225 230 235 240

Met Ser Arg Phe Cys Glu Ala Glu Phe Ser Val Lys Thr Arg Pro His
245 250 255

Trp Cys Cys Thr Arg Gln Gly Glu Ala Arg Phe Ser Cys Phe Gln Glu
260 265 270

Glu Ala Pro Gln Pro His Tyr Gln Leu Arg Ala Cys Pro Ser His Gln
275 280 285

Pro Asp Ile Ser Ser Gly Leu Glu Leu Pro Phe Pro Pro Gly Val Pro
290 295 300

Thr Leu Asp Asn Ile Lys Asn Ile Cys His Leu Arg Arg Phe Arg Ser
305 310 315 320

Val Pro Arg Asn Leu Pro Ala Thr Asp Pro Leu Gln Arg Glu Leu Leu
325 330 335

Ala Leu Ile Gln Leu Glu Arg Glu Phe Gln Arg Cys Cys Arg Gln Gly
340 345 350

Asn Asn His Thr Cys Thr Trp Lys Ala Trp Glu Asp Thr Leu Asp Lys
355 360 365

Tyr Cys Asp Arg Glu Tyr Ala Val Lys Thr His His His Leu Cys Cys

370

375

380

Arg His Pro Pro Ser Pro Thr Arg Asp Glu Cys Phe Ala Arg Arg Ala

385

390

395

400

Pro Tyr Pro Asn Tyr Asp Arg Asp Ile Leu Thr Ile Asp Ile Gly Arg

405

410

415

Val Thr Pro Asn Leu Met Gly His Leu Cys Gly Asn Gln Arg Val Leu

420

425

430

Thr Lys His Lys His Ile Pro Gly Leu Ile His Asn Met Thr Ala Arg

435

440

445

Cys Cys Asp Leu Pro Phe Pro Glu Gln Ala Cys Cys Ala Glu Glu Glu

450

455

460

Lys Leu Thr Phe Ile Asn Asp Leu Cys Gly Pro Arg Arg Asn Ile Trp

465

470

475

480

Arg Asp Pro Ala Leu Cys Cys Tyr Leu Ser Pro Gly Asp Glu Gln Val

485

490

495

Asn Cys Phe Asn Ile Asn Tyr Leu Arg Asn Val Ala Leu Val Ser Gly

500

505

510

Asp Thr Glu Asn Ala Lys Gly Gln Gly Glu Gln Gly Ser Thr Gly Gly

515

520

525

Thr Asn Ile Ser Ser Thr Ser Glu Pro Lys Glu Glu

530

535

540

<210> 110

<211> 1810

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (102).. (1721)

<400> 110

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gaggaccac ctcctgagtgt ccagtgggtca gttgccccag g atg ggg acc aca gcc 116

Met Gly Thr Thr Ala

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5

aga gca gcc ttg gtc ttg acc tat ttg gct gtt gct tct gct gcc tct 164

Arg Ala Ala Leu Val Leu Thr Tyr Leu Ala Val Ala Ser Ala Ala Ser

10

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gag gga ggc ttc acg gct aca gga cag agg cag ctg agg cca gag cac 212

Glu Gly Gly Phe Thr Ala Thr Gly Gln Arg Gln Leu Arg Pro Glu His

25

30

35

ttt caa gaa gtt ggc tac gca gct ccc ccc tcc cca ccc cta tcc cga 260

Phe Gln Glu Val Gly Tyr Ala Ala Pro Pro Ser Pro Pro Leu Ser Arg

40

45

50

agc ctc ccc atg gat cac cct gac tcc tct cag cat ggc cct ccc ttt 308

Ser Leu Pro Met Asp His Pro Asp Ser Ser Gln His Gly Pro Pro Phe

55

60

65

gag gga cag agt caa gtg cag ccc cct ccc tct cag gag gcc acc cct 356

Glu Gly Gln Ser Gln Val Gln Pro Pro Pro Ser Gln Glu Ala Thr Pro

70

75

80

85

ctc caa cag gaa aag ctg cta cct gcc caa ctc cct gct gaa aag gaa 404

Leu Gln Gln Glu Lys Leu Leu Pro Ala Gln Leu Pro Ala Glu Lys Glu

90

95

100

gtg ggt ccc cct ctc cct cag gaa gct gtc ccc ctc caa aaa gag ctg 452

Val Gly Pro Pro Leu Pro Gln Glu Ala Val Pro Leu Gln Lys Glu Leu

105

110

115

ccc tct ctc cag cac ccc aat gaa cag aag gaa gga acg cca gct cca 500

Pro Ser Leu Gln His Pro Asn Glu Gln Lys Glu Gly Thr Pro Ala Pro

120

125

130

ttt ggg gac cag agc cat cca gaa cct gag tcc tgg aat gca gcc cag 548

Phe Gly Asp Gln Ser His Pro Glu Pro Glu Ser Trp Asn Ala Ala Gln

135

140

145

cac tgc caa cag gac cgg tcc caa ggg ggc tgg ggc cac cgg ctg gat 596

His Cys Gln Gln Asp Arg Ser Gln Gly Gly Trp Gly His Arg Leu Asp

150

155

160

165

ggc ttc ccc cct ggg cgg cct tct cca gac aat ctg aac caa atc tgc 644

Gly Phe Pro Pro Gly Arg Pro Ser Pro Asp Asn Leu Asn Gln Ile Cys

170

175

180

ctt cct aac cgt cag cat gtg gta tat ggt ccc tgg aac cta cca cag 692

Leu Pro Asn Arg Gln His Val Val Tyr Gly Pro Trp Asn Leu Pro Gln

185

190

195

tcc agc tac tcc cac ctc act cgc cag ggt gag acc ctc aat ttc ctg 740

Ser Ser Tyr Ser His Leu Thr Arg Gln Gly Glu Thr Leu Asn Phe Leu

200

205

210

gag att gga tat tcc cgc tgc tgc cac tgc cgc agc cac aca aac cgc 788

Glu Ile Gly Tyr Ser Arg Cys Cys His Cys Arg Ser His Thr Asn Arg

215

220

225

cta gag tgt gcc aaa ctt gtg tgg gag gaa gca atg agc cga ttc tgt 836

Leu Glu Cys Ala Lys Leu Val Trp Glu Glu Ala Met Ser Arg Phe Cys

230

235

240

245

gag gcc gag ttc tcg gtc aag acc cga ccc cac tgg tgc tgc acg cgg 884

Glu Ala Glu Phe Ser Val Lys Thr Arg Pro His Trp Cys Cys Thr Arg

250

255

260

cag ggg gag gct cgg ttc tcc tgc ttc cag gag gaa gct ccc cag cca 932

Gln Gly Glu Ala Arg Phe Ser Cys Phe Gln Glu Glu Ala Pro Gln Pro
 265 270 275

cac tac cag ctc cgg gcc tgc ccc agc cat cag cct gat att tcc tcg 980
 His Tyr Gln Leu Arg Ala Cys Pro Ser His Gln Pro Asp Ile Ser Ser
 280 285 290

ggt ctt gag ctg cct ttc cct cct ggg gtg ccc aca ttg gac aat atc 1028
 Gly Leu Glu Leu Pro Phe Pro Pro Gly Val Pro Thr Leu Asp Asn Ile
 295 300 305

aag aac atc tgc cac ctg agg cgc ttc cgc tct gtg cca cgc aac ctg 1076
 Lys Asn Ile Cys His Leu Arg Arg Phe Arg Ser Val Pro Arg Asn Leu
 310 315 320 325

cca gct act gac ccc cta caa agg gag ctg ctg gca ctg atc cag ctg 1124
 Pro Ala Thr Asp Pro Leu Gln Arg Glu Leu Leu Ala Leu Ile Gln Leu
 330 335 340

gag agg gag ttc cag cgc tgc tgc cgc cag ggg aac aat cac acc tgt 1172
 Glu Arg Glu Phe Gln Arg Cys Cys Arg Gln Gly Asn Asn His Thr Cys
 345 350 355

aca tgg aag gcc tgg gag gat acc ctt gac aaa tac tgt gac cgg gag 1220
 Thr Trp Lys Ala Trp Glu Asp Thr Leu Asp Lys Tyr Cys Asp Arg Glu
 360 365 370

tat gct gtg aag acc cac cac cac ttg tgt tgc cgc cac cct ccc agc 1268
 Tyr Ala Val Lys Thr His His His Leu Cys Cys Arg His Pro Pro Ser

375

380

385

cct act cgg gat gag tgc ttt gcc cgt cgg gct cct tac ccc aac tat 1316

Pro Thr Arg Asp Glu Cys Phe Ala Arg Arg Ala Pro Tyr Pro Asn Tyr

390

395

400

405

gac cgg gac atc ttg acc att gac atc ggt cga gtc acc ccc aac ctc 1364

Asp Arg Asp Ile Leu Thr Ile Asp Ile Gly Arg Val Thr Pro Asn Leu

410

415

420

atg ggc cac ctc tgt gga aac caa aga gtt ctc acc aag cat aaa cat 1412

Met Gly His Leu Cys Gly Asn Gln Arg Val Leu Thr Lys His Lys His

425

430

435

att cct ggg ctg atc cac aac atg act gcc cgc tgc tgt gac ctg cca 1460

Ile Pro Gly Leu Ile His Asn Met Thr Ala Arg Cys Cys Asp Leu Pro

440

445

450

ttt cca gaa cag gcc tgc tgt gca gag gag gag aaa tta acc ttc atc 1508

Phe Pro Glu Gln Ala Cys Cys Ala Glu Glu Glu Lys Leu Thr Phe Ile

455

460

465

aat gat ctg tgt ggt ccc cga cgt aac atc tgg cga gac cct gcc ctc 1556

Asn Asp Leu Cys Gly Pro Arg Arg Asn Ile Trp Arg Asp Pro Ala Leu

470

475

480

485

tgc tgt tac ctg agt cct ggg gat gaa cag gtc aac tgc ttc aac atc 1604

Cys Cys Tyr Leu Ser Pro Gly Asp Glu Gln Val Asn Cys Phe Asn Ile

490

495

500

aat tat ctg agg aac gtg gct cta gtg tct gga gac act gag aac gcc 1652

Asn Tyr Leu Arg Asn Val Ala Leu Val Ser Gly Asp Thr Glu Asn Ala

505

510

515

aag ggc cag ggg gag cag ggc tca act gga gga aca aat atc agc tcc 1700

Lys Gly Gln Gly Glu Gln Gly Ser Thr Gly Gly Thr Asn Ile Ser Ser

520

525

530

acc tct gag ccc aag gaa gaa tgagtcacc cagagcccta gagggtcaga 1751

Thr Ser Glu Pro Lys Glu Glu

535

540

tggggggaac cccaccctgc cccacccatc tgaacactca ttacactaaa cacctcttg 1810

<210> 111

<211> 540

<212> PRT

<213> Homo sapiens

<400> 111

Met Gly Thr Thr Ala Arg Ala Ala Leu Val Leu Thr Tyr Leu Ala Val

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Ala Ser Ala Ala Ser Glu Gly Gly Phe Thr Ala Thr Gly Gln Arg Gln

20

25

30

Leu Arg Pro Glu His Phe Gln Glu Val Gly Tyr Ala Ala Pro Pro Ser

35

40

45

Pro Pro Leu Ser Arg Ser Leu Pro Met Asp His Pro Asp Ser Ser Gln

50

55

60

His Gly Pro Pro Phe Glu Gly Gln Ser Gln Val Gln Pro Pro Pro Ser

65

70

75

80

Gln Glu Ala Thr Pro Leu Gln Gln Glu Lys Leu Leu Pro Ala Gln Leu

85

90

95

Pro Ala Glu Lys Glu Val Gly Pro Pro Leu Pro Gln Glu Ala Val Pro

100

105

110

Leu Gln Lys Glu Leu Pro Ser Leu Gln His Pro Asn Glu Gln Lys Glu

115

120

125

Gly Thr Pro Ala Pro Phe Gly Asp Gln Ser His Pro Glu Pro Glu Ser

130

135

140

Trp Asn Ala Ala Gln His Cys Gln Gln Asp Arg Ser Gln Gly Gly Trp

145

150

155

160

Gly His Arg Leu Asp Gly Phe Pro Pro Gly Arg Pro Ser Pro Asp Asn

165

170

175

Leu Asn Gln Ile Cys Leu Pro Asn Arg Gln His Val Val Tyr Gly Pro

180

185

190

Trp Asn Leu Pro Gln Ser Ser Tyr Ser His Leu Thr Arg Gln Gly Glu
195 200 205

Thr Leu Asn Phe Leu Glu Ile Gly Tyr Ser Arg Cys Cys His Cys Arg
210 215 220

Ser His Thr Asn Arg Leu Glu Cys Ala Lys Leu Val Trp Glu Glu Ala
225 230 235 240

Met Ser Arg Phe Cys Glu Ala Glu Phe Ser Val Lys Thr Arg Pro His
245 250 255

Trp Cys Cys Thr Arg Gln Gly Glu Ala Arg Phe Ser Cys Phe Gln Glu
260 265 270

Glu Ala Pro Gln Pro His Tyr Gln Leu Arg Ala Cys Pro Ser His Gln
275 280 285

Pro Asp Ile Ser Ser Gly Leu Glu Leu Pro Phe Pro Pro Gly Val Pro
290 295 300

Thr Leu Asp Asn Ile Lys Asn Ile Cys His Leu Arg Arg Phe Arg Ser
305 310 315 320

Val Pro Arg Asn Leu Pro Ala Thr Asp Pro Leu Gln Arg Glu Leu Leu
325 330 335

Ala Leu Ile Gln Leu Glu Arg Glu Phe Gln Arg Cys Cys Arg Gln Gly
340 345 350

Asn Asn His Thr Cys Thr Trp Lys Ala Trp Glu Asp Thr Leu Asp Lys
355 360 365

Tyr Cys Asp Arg Glu Tyr Ala Val Lys Thr His His His Leu Cys Cys
370 375 380

Arg His Pro Pro Ser Pro Thr Arg Asp Glu Cys Phe Ala Arg Arg Ala
385 390 395 400

Pro Tyr Pro Asn Tyr Asp Arg Asp Ile Leu Thr Ile Asp Ile Ser Arg
405 410 415

Val Thr Pro Asn Leu Met Gly His Leu Cys Gly Asn Gln Arg Val Leu
420 425 430

Thr Lys His Lys His Ile Pro Gly Leu Ile His Asn Met Thr Ala Arg
435 440 445

Cys Cys Asp Leu Pro Phe Pro Glu Gln Ala Cys Cys Ala Glu Glu Glu
450 455 460

Lys Leu Thr Phe Ile Asn Asp Leu Cys Gly Pro Arg Arg Asn Ile Trp
465 470 475 480

Arg Asp Pro Ala Leu Cys Cys Tyr Leu Ser Pro Gly Asp Glu Gln Val
485 490 495

Asn Cys Phe Asn Ile Asn Tyr Leu Arg Asn Val Ala Leu Val Ser Gly

500

505

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Asp Thr Glu Asn Ala Lys Gly Gln Gly Glu Gln Gly Ser Thr Gly Gly

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Thr Asn Ile Ser Ser Thr Ser Glu Pro Lys Glu Glu

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<211> 1810

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> (102).. (1721)

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gaggaccac ctctgagtgt ccagtggica gttgccccag g atg ggg acc aca gcc 116

Met Gly Thr Thr Ala

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aga gca gcc ttg gtc ttg acc tat ttg gct gtt gct tct gct gcc tct 164

Arg Ala Ala Leu Val Leu Thr Tyr Leu Ala Val Ala Ser Ala Ala Ser

10

15

20

gag gga ggc ttc acg gct aca gga cag agg cag ctg agg cca gag cac 212

Glu Gly Gly Phe Thr Ala Thr Gly Gln Arg Gln Leu Arg Pro Glu His

25

30

35

ttt caa gaa gtt ggc tac gca gct ccc ccc tcc cca ccc cta tcc cga 260

Phe Gln Glu Val Gly Tyr Ala Ala Pro Pro Ser Pro Pro Leu Ser Arg

40

45

50

agc ctc ccc atg gat cac cct gac tcc tct cag cat ggc cct ccc ttt 308

Ser Leu Pro Met Asp His Pro Asp Ser Ser Gln His Gly Pro Pro Phe

55

60

65

gag gga cag agt caa gtg cag ccc cct ccc tct cag gag gcc acc cct 356

Glu Gly Gln Ser Gln Val Gln Pro Pro Pro Ser Gln Glu Ala Thr Pro

70

75

80

85

ctc caa cag gaa aag ctg cta cct gcc caa ctc cct gct gaa aag gaa 404

Leu Gln Gln Glu Lys Leu Leu Pro Ala Gln Leu Pro Ala Glu Lys Glu

90

95

100

gtg ggt ccc cct ctc cct cag gaa gct gtc ccc ctc caa aaa gag ctg 452

Val Gly Pro Pro Leu Pro Gln Glu Ala Val Pro Leu Gln Lys Glu Leu

105

110

115

ccc tct ctc cag cac ccc aat gaa cag aag gaa gga acg cca gct cca 500

Pro Ser Leu Gln His Pro Asn Glu Gln Lys Glu Gly Thr Pro Ala Pro

120

125

130

ttt ggg gac cag agc cat cca gaa cct gag tcc tgg aat gca gcc cag 548

Phe Gly Asp Gln Ser His Pro Glu Pro Glu Ser Trp Asn Ala Ala Gln

135

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cac tgc caa cag gac cgg tcc caa ggg ggc tgg ggc cac cgg ctg gat 596

His Cys Gln Gln Asp Arg Ser Gln Gly Gly Trp Gly His Arg Leu Asp

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155

160

165

ggc ttc ccc cct ggg cgg cct tct cca gac aat ctg aac caa atc tgc 644

Gly Phe Pro Pro Gly Arg Pro Ser Pro Asp Asn Leu Asn Gln Ile Cys

170

175

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ctt cct aac cgt cag cat gtg gta tat ggt ccc tgg aac cta cca cag 692

Leu Pro Asn Arg Gln His Val Val Tyr Gly Pro Trp Asn Leu Pro Gln

185

190

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tcc agc tac tcc cac ctc act cgc cag ggt gag acc ctc aat ttc ctg 740

Ser Ser Tyr Ser His Leu Thr Arg Gln Gly Glu Thr Leu Asn Phe Leu

200

205

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gag att gga tat tcc cgc tgc tgc cac tgc cgc agc cac aca aac cgc 788

Glu Ile Gly Tyr Ser Arg Cys Cys His Cys Arg Ser His Thr Asn Arg

215

220

225

cta gag tgt gcc aaa ctt gtg tgg gag gaa gca atg agc cga ttc tgt 836

Leu Glu Cys Ala Lys Leu Val Trp Glu Glu Ala Met Ser Arg Phe Cys

230

235

240

245

gag gcc gag ttc tgc gtc aag acc cga ccc cac tgg tgc tgc acg cgg 884

Glu Ala Glu Phe Ser Val Lys Thr Arg Pro His Trp Cys Cys Thr Arg

250

255

260

cag ggg gag gct cgg ttc tcc tgc ttc cag gag gaa gct ccc cag cca 932

Gln Gly Glu Ala Arg Phe Ser Cys Phe Gln Glu Glu Ala Pro Gln Pro

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cac tac cag ctc cgg gcc tgc ccc agc cat cag cct gat att tcc tgc 980

His Tyr Gln Leu Arg Ala Cys Pro Ser His Gln Pro Asp Ile Ser Ser

280

285

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ggt ctt gag ctg cct ttc cct cct ggg gtg ccc aca ttg gac aat atc 1028

Gly Leu Glu Leu Pro Phe Pro Pro Gly Val Pro Thr Leu Asp Asn Ile

295

300

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aag aac atc tgc cac ctg agg cgc ttc cgc tct gtg cca cgc aac ctg 1076

Lys Asn Ile Cys His Leu Arg Arg Phe Arg Ser Val Pro Arg Asn Leu

310

315

320

325

cca gct act gac ccc cta caa agg gag ctg ctg gca ctg atc cag ctg 1124

Pro Ala Thr Asp Pro Leu Gln Arg Glu Leu Leu Ala Leu Ile Gln Leu

330

335

340

gag agg gag ttc cag cgc tgc tgc cgc cag ggg aac aat cac acc tgt 1172

Glu Arg Glu Phe Gln Arg Cys Cys Arg Gln Gly Asn Asn His Thr Cys

345

350

355

aca tgg aag gcc tgg gag gat acc ctt gac aaa tac tgt gac cgg gag 1220

Thr Trp Lys Ala Trp Glu Asp Thr Leu Asp Lys Tyr Cys Asp Arg Glu

360

365

370

tat gct gtg aag acc cac cac cac ttg tgt tgc cgc cac cct ccc agc 1268

Tyr Ala Val Lys Thr His His His Leu Cys Cys Arg His Pro Pro Ser

375

380

385

cct act cgg gat gag tgc ttt gcc cgt cgg gct cct tac ccc aac tat 1316

Pro Thr Arg Asp Glu Cys Phe Ala Arg Arg Ala Pro Tyr Pro Asn Tyr

390

395

400

405

gac cgg gac atc ttg acc att gac atc agt cga gtc acc ccc aac ctc 1364

Asp Arg Asp Ile Leu Thr Ile Asp Ile Ser Arg Val Thr Pro Asn Leu

410

415

420

atg ggc cac ctc tgt gga aac caa aga gtt ctc acc aag cat aaa cat 1412

Met Gly His Leu Cys Gly Asn Gln Arg Val Leu Thr Lys His Lys His

425

430

435

att cct ggg ctg atc cac aac atg act gcc cgc tgc tgt gac ctg cca 1460

Ile Pro Gly Leu Ile His Asn Met Thr Ala Arg Cys Cys Asp Leu Pro

440

445

450

ttt cca gaa cag gcc tgc tgt gca gag gag gag aaa tta acc ttc atc 1508

Phe Pro Glu Gln Ala Cys Cys Ala Glu Glu Glu Lys Leu Thr Phe Ile

455

460

465

aat gat ctg tgt ggt ccc cga cgt aac atc tgg cga gac cct gcc ctc 1556

Asn Asp Leu Cys Gly Pro Arg Arg Asn Ile Trp Arg Asp Pro Ala Leu

470

475

480

485

tgc tgt tac ctg agt cct ggg gat gaa cag gtc aac tgc ttc aac atc 1604

Cys Cys Tyr Leu Ser Pro Gly Asp Glu Gln Val Asn Cys Phe Asn Ile

490

495

500

aat tat ctg agg aac gtg gct cta gtg tct gga gac act gag aac gcc 1652

Asn Tyr Leu Arg Asn Val Ala Leu Val Ser Gly Asp Thr Glu Asn Ala

505

510

515

aag ggc cag ggg gag cag ggc tca act gga gga aca aat atc agc tcc 1700

Lys Gly Gln Gly Glu Gln Gly Ser Thr Gly Gly Thr Asn Ile Ser Ser

520

525

530

acc tct gag ccc aag gaa gaa tgagtcaccc cagagcccta gagggtcaga 1751

Thr Ser Glu Pro Lys Glu Glu

535

540

tggggggaac cccaccctgc cccaccctgc tgaacactca ttācactaaa cacctcttg 1810

<210> 113

<211> 382

<212> PRT

<213> Homo sapiens

<400> 113

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Tyr Ser Thr Ala Gly Gly Lys Val Trp Leu Ser Val Leu Phe Ile Phe

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Arg Ile Leu Leu Leu Gly Thr Ala Val Glu Ser Ala Trp Gly Asp Glu		
35	40	45
Gln Ser Ala Phe Arg Cys Asn Thr Gln Gln Pro Gly Cys Glu Asn Val		
50	55	60
Cys Tyr Asp Lys Ser Phe Pro Ile Ser His Val Arg Phe Trp Val Leu		
65	70	75 80
Gln Ile Ile Phe Val Ser Val Pro Thr Leu Leu Tyr Leu Ala His Val		
85	90	95
Phe Tyr Val Met Arg Lys Glu Glu Lys Leu Asn Lys Lys Glu Glu Glu		
100	105	110
Leu Lys Val Ala Gln Thr Asp Gly Val Asn Val Asp Met His Leu Lys		
115	120	125
Gln Ile Glu Ile Lys Lys Phe Lys Tyr Gly Ile Glu Glu His Gly Lys		
130	135	140
Val Lys Met Arg Gly Gly Leu Leu Arg Thr Tyr Ile Ile Ser Ile Leu		
145	150	155 160
Phe Lys Ser Ile Phe Glu Val Ala Phe Leu Leu Ile Gln Trp Tyr Ile		
165	170	175

Tyr Gly Phe Ser Leu Ser Ala Val Tyr Thr Cys Lys Arg Asp Pro Cys
180 185 190

Pro His Gln Val Asp Cys Phe Leu Ser Arg Pro Thr Glu Lys Thr Ile
195 200 205

Phe Ile Ile Phe Met Leu Val Val Ser Leu Val Ser Leu Ala Leu Asn
210 215 220

Ile Ile Glu Leu Phe Tyr Val Phe Phe Lys Gly Val Lys Asp Arg Val
225 230 235 240

Lys Gly Lys Ser Asp Pro Tyr His Ala Thr Ser Gly Ala Leu Ser Pro
245 250 255

Ala Lys Asp Cys Gly Ser Gln Lys Tyr Ala Tyr Phe Asn Gly Cys Ser
260 265 270

Ser Pro Thr Ala Pro Leu Ser Pro Met Ser Pro Pro Gly Tyr Lys Leu
275 280 285

Val Thr Gly Asp Arg Asn Asn Ser Ser Cys Arg Asn Tyr Asn Lys Gln
290 295 300

Ala Ser Glu Gln Thr Trp Ala Asn Tyr Ser Ala Glu Gln Asn Arg Met
305 310 315 320

Gly Gln Ala Gly Ser Thr Ile Ser Asn Ser His Ala Gln Pro Phe Asp
325 330 335

Phe Pro Asp Asp Asn Gln Asn Ser Lys Lys Leu Ala Ala Gly His Glu

340

345

350

Leu Gln Pro Leu Ala Ile Val Asp Gln Arg Pro Ser Ser Arg Ala Ser

355

360

365

Ser Arg Ala Ser Ser Arg Pro Arg Pro Asp Asp Leu Glu Ile

370

375

380

<210> 114

<211> 3074

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (201).. (1346)

<400> 114

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aacagcagcg gagtttttaa ctttaaatac acaggtctga gtcctgaac ttgccttttc 120

attttacttc atcctccaag gagttcaatc acttggcgtg acttactac ttttaagcaa 180

aagagtgggtg cccaggcaac atg ggt gac tgg agc gcc tta ggc aaa ctc ctt 233

Met Gly Asp Trp Ser Ala Leu Gly Lys Leu Leu

1

5

10

gac aag gtt caa gcc tac tca act gct gga ggg aag gtg tgg ctg tca 281

Asp Lys Val Gln Ala Tyr Ser Thr Ala Gly Gly Lys Val Trp Leu Ser

15

20

25

gta ctt ttc att ttc cga atc ctg ctg ctg ggg aca gcg gtt gag tca 329

Val Leu Phe Ile Phe Arg Ile Leu Leu Leu Gly Thr Ala Val Glu Ser

30

35

40

gcc tgg gga gat gag cag tct gcc ttt cgt tgt aac act cag caa cct 377

Ala Trp Gly Asp Glu Gln Ser Ala Phe Arg Cys Asn Thr Gln Gln Pro

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55

ggc tgt gaa aat gtc tgc tat gac aag tct ttc cca atc tct cat gtg 425

Gly Cys Glu Asn Val Cys Tyr Asp Lys Ser Phe Pro Ile Ser His Val

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65

70

75

cgc ttc tgg gtc ctg cag atc ata ttt gtg tct gta ccc aca ctc ttg 473

Arg Phe Trp Val Leu Gln Ile Ile Phe Val Ser Val Pro Thr Leu Leu

80

85

90

tac ctg gct cat gtg ttc tat gtg atg cga aag gaa gag aaa ctg aac 521

Tyr Leu Ala His Val Phe Tyr Val Met Arg Lys Glu Glu Lys Leu Asn

95

100

105

aag aaa gag gaa gaa ctc aag gtt gcc caa act gat ggt gtc aat gtg 569

Lys Lys Glu Glu Glu Leu Lys Val Ala Gln Thr Asp Gly Val Asn Val

110

115

120

gac atg cac ttg aag cag att gag ata aag aag ttc aag tac ggt att 617

Asp Met His Leu Lys Gln Ile Glu Ile Lys Lys Phe Lys Tyr Gly Ile

125

130

135

gaa gag cat ggt aag gtg aaa atg cga ggg ggg ttg ctg cga acc tac 665

Glu Glu His Gly Lys Val Lys Met Arg Gly Gly Leu Leu Arg Thr Tyr

140

145

150

155

atc atc agt atc ctc ttc aag tct atc ttt gag gtg gcc ttc ttg ctg 713

Ile Ile Ser Ile Leu Phe Lys Ser Ile Phe Glu Val Ala Phe Leu Leu

160

165

170

atc cag tgg tac atc tat gga ttc agc ttg agt gct gtt tac act tgc 761

Ile Gln Trp Tyr Ile Tyr Gly Phe Ser Leu Ser Ala Val Tyr Thr Cys

175

180

185

aaa aga gat ccc tgc cca cat cag gtg gac tgt ttc ctc tct cgc ccc 809

Lys Arg Asp Pro Cys Pro His Gln Val Asp Cys Phe Leu Ser Arg Pro

190

195

200

acg gag aaa acc atc ttc atc atc ttc atg ctg gtg gtg tcc ttg gtg 857

Thr Glu Lys Thr Ile Phe Ile Ile Phe Met Leu Val Val Ser Leu Val

205

210

215

tcc ctg gcc ttg aat atc att gaa ctc ttc tat gtt ttc ttc aag ggc 905

Ser Leu Ala Leu Asn Ile Ile Glu Leu Phe Tyr Val Phe Phe Lys Gly

220

225

230

235

gtt aag gat cgg gtt aag gga aag agc gac cct tac cat gcg acc agt 953

Val Lys Asp Arg Val Lys Gly Lys Ser Asp Pro Tyr His Ala Thr Ser

240

245

250

ggt gcg ctg agc cct gcc aaa gac tgt ggg tct caa aaa tat gct tat 1001

Gly Ala Leu Ser Pro Ala Lys Asp Cys Gly Ser Gln Lys Tyr Ala Tyr

255

260

265

ttc aat ggc tgc tcc tca cca acc gct ccc ctc tgc cct atg tct cct 1049

Phe Asn Gly Cys Ser Ser Pro Thr Ala Pro Leu Ser Pro Met Ser Pro

270

275

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cct ggg tac aag ctg gtt act ggc gac aga aac aat tct tct tgc cgc 1097

Pro Gly Tyr Lys Leu Val Thr Gly Asp Arg Asn Asn Ser Ser Cys Arg

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290

295

aat tac aac aag caa gca agt gag caa acc tgg gct aat tac agt gca 1145

Asn Tyr Asn Lys Gln Ala Ser Glu Gln Thr Trp Ala Asn Tyr Ser Ala

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305

310

315

gaa caa aat cga atg ggg cag gcg gga agc acc atc tct aac tcc cat 1193

Glu Gln Asn Arg Met Gly Gln Ala Gly Ser Thr Ile Ser Asn Ser His

320

325

330

gca cag cct ttt gat ttc ccc gat gat aac cag aat tct aaa aaa cta 1241

Ala Gln Pro Phe Asp Phe Pro Asp Asp Asn Gln Asn Ser Lys Lys Leu

335

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345

gct gct gga cat gaa tta cag cca cta gcc att gtg gac cag cga cct 1289

Ala Ala Gly His Glu Leu Gln Pro Leu Ala Ile Val Asp Gln Arg Pro
350 355 360

tca agc aga gcc agc agt cgt gcc agc agc aga cct cgg cct gat gac 1337
Ser Ser Arg Ala Ser Ser Arg Ala Ser Ser Arg Pro Arg Pro Asp Asp
365 370 375

ctg gag atc tagatacagg ctgaaagca tcaagattcc actcaattgt 1386
Leu Glu Ile
380

ggagaagaaa aaaggctctg tagaaagtc accagggtgtt aattttgac cgggtggaggt 1446

ggtactcaac agccttattc atgaggctta gaaaacacaa agacattaga atacctaggt 1506

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cagtttctcc aaatgcccttt tttaaaactc atcacagaag attggtgaaa atgctgagta 2886

tgacactttt cttcttgcat gcatgtcagc tacataaaca gttttgtaca atgaaaatta 2946

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<212> PRT

<213> Homo sapiens

<400> 115

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15

Tyr Ser Thr Ala Gly Gly Lys Val Trp Leu Ser Val Leu Phe Ile Phe

20

25

30

Arg Ile Leu Leu Leu Gly Thr Ala Val Glu Ser Ala Trp Gly Asp Glu

35

40

45

Gln Ser Ala Phe Arg Cys Asn Thr Gln Gln Pro Gly Cys Glu Asn Val

50

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60

Cys Tyr Asp Lys Ser Phe Pro Ile Ser His Val Arg Phe Trp Val Leu
65 70 75 80

Gln Ile Ile Phe Val Ser Val Pro Thr Leu Leu Tyr Leu Ala His Val
85 90 95

Phe Tyr Val Met Arg Lys Glu Glu Lys Leu Asn Lys Lys Glu Glu Glu
100 105 110

Leu Lys Val Ala Gln Thr Asp Gly Val Asn Val Asp Met His Leu Lys
115 120 125

Gln Ile Glu Ile Lys Lys Phe Lys Tyr Gly Ile Glu Glu His Gly Lys
130 135 140

Val Lys Met Arg Gly Gly Leu Leu Arg Thr Tyr Ile Ile Ser Ile Leu
145 150 155 160

Phe Lys Ser Ile Phe Glu Val Ala Phe Leu Leu Ile Gln Trp Tyr Ile
165 170 175

Tyr Gly Phe Ser Leu Ser Ala Val Tyr Thr Cys Lys Arg Asp Pro Cys
180 185 190

Pro His Gln Val Asp Cys Phe Leu Ser Arg Pro Thr Glu Lys Thr Ile
195 200 205

Phe Ile Ile Phe Met Leu Val Val Ser Leu Val Ser Leu Ala Leu Asn

210	215	220	
Ile Ile Glu Leu Phe Tyr Val Phe Phe Lys Gly Val Lys Asp Arg Val			
225	230	235	240
Lys Gly Lys Ser Asp Pro Tyr His Ala Thr Ser Gly Ala Leu Ser Pro			
245	250	255	
Ala Lys Asp Cys Gly Ser Gln Lys Tyr Ala Tyr Phe Asn Gly Cys Ser			
260	265	270	
Ser Pro Thr Ala Pro Leu Ser Pro Met Ser Pro Pro Gly Tyr Lys Leu			
275	280	285	
Val Thr Gly Asp Arg Asn Asn Ser Ser Cys Arg Asn Tyr Asn Lys Gln			
290	295	300	
Ala Ser Glu Gln Asn Trp Ala Asn Tyr Ser Ala Glu Gln Asn Arg Met			
305	310	315	320
Gly Gln Ala Gly Ser Thr Ile Ser Asn Ser His Ala Gln Pro Phe Asp			
325	330	335	
Phe Pro Asp Asp Asn Gln Asn Ser Lys Lys Leu Ala Ala Gly His Glu			
340	345	350	
Leu Gln Pro Leu Ala Ile Val Asp Gln Arg Pro Ser Ser Arg Ala Ser			
355	360	365	

Ser Arg Ala Ser Ser Arg Pro Arg Pro Asp Asp Leu Glu Ile

370

375

380

<210> 116

<211> 3074

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (201).. (1346)

<400> 116

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attttacttc atcctccaag gagttcaatc acttggcgtg acttcactac tttaagcaa 180

aagagtggcg cccaggcaac atg ggt gac tgg agc gcc tta ggc aaa ctc ctt 233

Met Gly Asp Trp Ser Ala Leu Gly Lys Leu Leu

1

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10

gac aag gtt caa gcc tac tca act gct gga ggg aag gtg tgg ctg tca 281

Asp Lys Val Gln Ala Tyr Ser Thr Ala Gly Gly Lys Val Trp Leu Ser

15

20

25

gta ctt ttc att ttc cga atc ctg ctg ctg ggg aca gcg gtt gag tca 329

Val Leu Phe Ile Phe Arg Ile Leu Leu Leu Gly Thr Ala Val Glu Ser
 30 35 40

gcc tgg gga gat gag cag tct gcc ttt cgt tgt aac act cag caa cct 377
 Ala Trp Gly Asp Glu Gln Ser Ala Phe Arg Cys Asn Thr Gln Gln Pro
 45 50 55

ggi tgt gaa aat gtc tgc tat gac aag tct ttc cca atc tct cat gtg 425
 Gly Cys Glu Asn Val Cys Tyr Asp Lys Ser Phe Pro Ile Ser His Val
 60 65 70 75

cgc ttc tgg gtc ctg cag atc ata ttt gtg tct gta ccc aca ctc ttg 473
 Arg Phe Trp Val Leu Gln Ile Ile Phe Val Ser Val Pro Thr Leu Leu
 80 85 90

tac ctg gct cat gtg ttc tat gtg atg cga aag gaa gag aaa ctg aac 521
 Tyr Leu Ala His Val Phe Tyr Val Met Arg Lys Glu Glu Lys Leu Asn
 95 100 105

aag aaa gag gaa gaa ctc aag gtt gcc caa act gat ggt gtc aat gtg 569
 Lys Lys Glu Glu Glu Leu Lys Val Ala Gln Thr Asp Gly Val Asn Val
 110 115 120

gac atg cac ttg aag cag att gag ata aag aag ttc aag tac ggt att 617
 Asp Met His Leu Lys Gln Ile Glu Ile Lys Lys Phe Lys Tyr Gly Ile
 125 130 135

gaa gag cat ggt aag gtg aaa atg cga ggg ggg ttg ctg cga acc tac 665
 Glu Glu His Gly Lys Val Lys Met Arg Gly Gly Leu Leu Arg Thr Tyr

140	145	150	155	
atc atc agt atc ctc ttc aag tct atc ttt gag gtg gcc ttc ttg ctg				713
Ile Ile Ser Ile Leu Phe Lys Ser Ile Phe Glu Val Ala Phe Leu Leu				
	160	165	170	
atc cag tgg tac atc tat gga ttc agc ttg agt gct gtt tac act tgc				761
Ile Gln Trp Tyr Ile Tyr Gly Phe Ser Leu Ser Ala Val Tyr Thr Cys				
	175	180	185	
aaa aga gat ccc tgc cca cat cag gtg gac tgt ttc ctc tct cgc ccc				809
Lys Arg Asp Pro Cys Pro His Gln Val Asp Cys Phe Leu Ser Arg Pro				
	190	195	200	
acg gag aaa acc atc ttc atc atc ttc atg ctg gtg gtg tcc ttg gtg				857
Thr Glu Lys Thr Ile Phe Ile Ile Phe Met Leu Val Val Ser Leu Val				
	205	210	215	
tcc ctg gcc ttg aat atc att gaa ctc ttc tat gtt ttc ttc aag ggc				905
Ser Leu Ala Leu Asn Ile Ile Glu Leu Phe Tyr Val Phe Phe Lys Gly				
220	225	230	235	
gtt aag gat cgg gtt aag gga aag agc gac cct tac cat gcg acc agt				953
Val Lys Asp Arg Val Lys Gly Lys Ser Asp Pro Tyr His Ala Thr Ser				
	240	245	250	
ggc gcg ctg agc cct gcc aaa gac tgt ggg tct caa aaa tat gct tat				1001
Gly Ala Leu Ser Pro Ala Lys Asp Cys Gly Ser Gln Lys Tyr Ala Tyr				
	255	260	265	

ttc aat ggc tgc tcc tca cca acc gct ccc ctc tcg cct atg tct cct 1049

Phe Asn Gly Cys Ser Ser Pro Thr Ala Pro Leu Ser Pro Met Ser Pro

270

275

280

cct ggg tac aag ctg gtt act ggc gac aga aac aat tct tct tgc cgc 1097

Pro Gly Tyr Lys Leu Val Thr Gly Asp Arg Asn Asn Ser Ser Cys Arg

285

290

295

aat tac aac aag caa gca agt gag caa aac tgg gct aat tac agt gca 1145

Asn Tyr Asn Lys Gln Ala Ser Glu Gln Asn Trp Ala Asn Tyr Ser Ala

300

305

310

315

gaa caa aat cga atg ggg cag gcg gga agc acc atc tct aac tcc cat 1193

Glu Gln Asn Arg Met Gly Gln Ala Gly Ser Thr Ile Ser Asn Ser His

320

325

330

gca cag cct ttt gat ttc ccc gat gat aac cag aat tct aaa aaa cta 1241

Ala Gln Pro Phe Asp Phe Pro Asp Asp Asn Gln Asn Ser Lys Lys Leu

335

340

345

gct gct gga cat gaa tta cag cca cta gcc att gtg gac cag cga cct 1289

Ala Ala Gly His Glu Leu Gln Pro Leu Ala Ile Val Asp Gln Arg Pro

350

355

360

tca agc aga gcc agc agt cgt gcc agc agc aga cct cgg cct gat gac 1337

Ser Ser Arg Ala Ser Ser Arg Ala Ser Ser Arg Pro Arg Pro Asp Asp

365

370

375

ctg gag atc tagatacagg ctgaaagca tcaagattcc actcaattgt 1386

Leu Glu Ile

380

ggagaagaaa aaagggtgctg tagaaagtgc accagggtgtt aattttgatc cgggtggaggt 1446

ggtactcaac agccttattc atgaggctta gaaaacacaa agacattaga atacctaggt 1506

tcactggggg tgtatggggt agatgggtgg agaggagagg gataagagag gtgcatgttg 1566

gtatttaaag tagtggattc aaagaacita gattataaat aagagtcca ttaggtgata 1626

catagataag ggctttttct ccccgcaaac acccctaaga atggttctgt gtatgtgaat 1686

gagcgggtgg taattgtggc taaatatitt tgttttacca agaaactgaa ataattctgg 1746

ccaggaataa atacttcctg aacatcttag gtcttttcaa caagaaaaag acagaggatt 1806

gtccttaagt ccttgctaaa acattccatt gttaaaattt gcacttigaa ggtaagcttt 1866

ctaggcctga cctccaggt gtcaatggac ttgtgctact atattttttt attcttggtg 1926

tcagtttaaa attcagacaa ggcccacaga ataagatttt ccatgcattt gcaaatacgt 1986

atattctttt tccatccact tgcacaatat cattaccatc actttttcat cattcctcag 2046

ctactactca cattcattta atggtttctg taaacatttt taagacagtt gggatgtcac 2106

ttaacatttt ttttttgagc taaagtcagg gaatcaagcc atgcittaata ttttaacaatc 2166

actatattgt gtgtcgaaga gtttgttttg tttgtcatgt attggtacaa gcagatacag 2226

tataaactca caaacacaga ttigaaaata atgcacatat ggtgttcaaa ttigaacctt 2286

tctcatggat ttttgtggig tgggccaata tgggttttac attatataat tctgtctgtg 2346

gcaagtaaag cacacttttt tttcttcta aaatgttttt cctgtgtat cctattaagg 2406

atactggitt tgttaattat gattctttat tttcttctt ttttttagga tatagcagta 2466

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gaattttagt actgtaaaca ggcttttagtc attaatgiga gagacttaga aaaaaatgct 2586

tagagtggac tattaatgt gcctaaatga attttgcagt aactgggtatt cttgggtttt 2646

cctacttaat acacagtaat tcagaacttg tattctatta tgagtttagc agtcttttgg 2706

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agaggattca gtagtacaca tacaactaat ttatttgaac tatatgttga agacatctac 2826

cagtttctcc aaatgccitt tttaaaactc atcacagaag attggtgaaa atgctgagta 2886

tgacactttt ctcttgcgt gcatgtcagc tacataaaca gttttgtaca atgaaaatta 2946

ctaatttgtt tgacattcca tgttaaacta cggtcatggt cagcttcatt gcatgtaatg 3006

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tttagtat

3074

<210> 117

<211> 398

<212> PRT

<213> Homo sapiens

<400> 117

Met Glu Gly Ala Ala Leu Leu Arg Val Ser Val Leu Cys Ile Trp Met

1

5

10

15

Ser Ala Leu Phe Leu Gly Val Gly Val Arg Ala Glu Glu Ala Gly Ala

20

25

30

Arg Val Gln Gln Asn Val Pro Ser Gly Thr Asp Thr Gly Asp Pro Gln

35

40

45

Ser Lys Pro Leu Gly Asp Trp Ala Ala Gly Thr Met Asp Pro Glu Ser

50

55

60

Ser Ile Phe Ile Glu Asp Ala Ile Lys Tyr Phe Lys Glu Lys Val Ser

65

70

75

80

Thr Gln Asn Leu Leu Leu Leu Thr Asp Asn Glu Ala Trp Asn Gly

85

90

95

Phe Val Ala Ala Ala Glu Leu Pro Arg Asn Glu Ala Asp Glu Leu Arg

100

105

110

Lys Ala Leu Asp Asn Leu Ala Arg Gln Met Ile Met Lys Asp Lys Asn

115

120

125

Trp His Asp Lys Gly Gln Gln Tyr Arg Asn Trp Phe Leu Lys Glu Phe

130

135

140

Pro Arg Leu Lys Ser Lys Leu Glu Asp Asn Ile Arg Arg Leu Arg Ala

145

150

155

160

Leu Ala Asp Gly Val Gln Lys Val His Lys Gly Thr Thr Ile Ala Asn

165

170

175

Val Val Ser Gly Ser Leu Ser Ile Ser Ser Gly Ile Leu Thr Leu Val

180

185

190

Gly Met Gly Leu Ala Pro Phe Thr Glu Gly Gly Ser Leu Val Leu Leu

195

200

205

Glu Pro Gly Met Glu Leu Gly Ile Thr Ala Ala Leu Thr Gly Ile Thr

210

215

220

Ser Ser Thr Ile Asp Tyr Gly Lys Lys Trp Trp Thr Gln Ala Gln Ala

225

230

235

240

His Asp Leu Val Ile Lys Ser Leu Asp Lys Leu Lys Glu Val Lys Glu

245

250

255

Phe Leu Gly Glu Asn Ile Ser Asn Phe Leu Ser Leu Ala Gly Asn Thr
260 265 270

Tyr Gln Leu Thr Arg Gly Ile Gly Lys Asp Ile Arg Ala Leu Arg Arg
275 280 285

Ala Arg Ala Asn Leu Gln Ser Val Pro His Ala Ser Ala Ser Arg Pro
290 295 300

Arg Val Thr Glu Pro Ile Ser Ala Glu Ser Gly Glu Gln Val Glu Arg
305 310 315 320

Val Asn Glu Pro Ser Ile Leu Glu Met Ser Arg Gly Val Lys Leu Thr
325 330 335

Asp Val Ala Pro Val Ser Phe Phe Leu Val Leu Asp Val Val Tyr Leu
340 345 350

Val Tyr Glu Ser Lys His Leu His Glu Gly Ala Lys Ser Glu Thr Ala
355 360 365

Glu Glu Leu Lys Lys Val Ala Gln Glu Leu Glu Glu Lys Leu Asn Ile
370 375 380

Leu Asn Asn Asn Tyr Lys Ile Leu Gln Ala Asp Gln Glu Leu
385 390 395

<210> 118

<211> 2054

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (76).. (1269)

<400> 118

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aggccctgca gcgac atg gag gga gct gct ttg ctg aga gtc tct gtc ctc 111

Met Glu Gly Ala Ala Leu Leu Arg Val Ser Val Leu

1

5

10

tgc atc tgg atg agt gca ctt ttc ctt ggt gtg gga gtg agg gca gag 159

Cys Ile Trp Met Ser Ala Leu Phe Leu Gly Val Gly Val Arg Ala Glu

15

20

25

gaa gct gga gcg agg gtg caa caa aac gtt cca agt ggg aca gat act 207

Glu Ala Gly Ala Arg Val Gln Gln Asn Val Pro Ser Gly Thr Asp Thr

30

35

40

gga gat cct caa agt aag ccc ctc ggt gac tgg gct gct ggc acc atg 255

Gly Asp Pro Gln Ser Lys Pro Leu Gly Asp Trp Ala Ala Gly Thr Met

45

50

55

60

gac cca gag agc agt atc ttt att gag gat gcc att aag tat ttc aag 303

Asp Pro Glu Ser Ser Ile Phe Ile Glu Asp Ala Ile Lys Tyr Phe Lys

65

70

75

gaa aaa gtg agc aca cag aat ctg cta ctc ctg ctg act gat aat gag 351

Glu Lys Val Ser Thr Gln Asn Leu Leu Leu Leu Leu Thr Asp Asn Glu

80

85

90

gcc tgg aac gga ttc gtg gct gct gct gaa ctg ccc agg aat gag gca 399

Ala Trp Asn Gly Phe Val Ala Ala Ala Glu Leu Pro Arg Asn Glu Ala

95

100

105

gat gag ctc cgt aaa gct ctg gac aac ctt gca aga caa atg atc atg 447

Asp Glu Leu Arg Lys Ala Leu Asp Asn Leu Ala Arg Gln Met Ile Met

110

115

120

aaa gac aaa aac tgg cac gat aaa ggc cag cag tac aga aac tgg ttt 495

Lys Asp Lys Asn Trp His Asp Lys Gly Gln Gln Tyr Arg Asn Trp Phe

125

130

135

140

ctg aaa gag ttt cct cgg ttg aaa agt aag ctt gag gat aac ata aga 543

Leu Lys Glu Phe Pro Arg Leu Lys Ser Lys Leu Glu Asp Asn Ile Arg

145

150

155

agg ctc cgt gcc ctt gca gat ggg gtt cag aag gtc cac aaa ggc acc 591

Arg Leu Arg Ala Leu Ala Asp Gly Val Gln Lys Val His Lys Gly Thr

160

165

170

acc atc gcc aat gtg gtg tct ggc tct ctc agc att tcc tct ggc atc 639

Thr Ile Ala Asn Val Val Ser Gly Ser Leu Ser Ile Ser Ser Gly Ile

175	180	185	
ctg acc ctc gtc ggc atg ggt ctg gca ccc ttc aca gag gga ggc agc			687
Leu Thr Leu Val Gly Met Gly Leu Ala Pro Phe Thr Glu Gly Gly Ser			
190	195	200	
ctt gta ctc ttg gaa cct ggg atg gag ttg gga atc aca gca gct ttg			735
Leu Val Leu Leu Glu Pro Gly Met Glu Leu Gly Ile Thr Ala Ala Leu			
205	210	215	220
acc ggg att acc agc agt acc ata gac tac gga aag aag tgg tgg aca			783
Thr Gly Ile Thr Ser Ser Thr Ile Asp Tyr Gly Lys Lys Trp Trp Thr			
225	230	235	
caa gcc caa gcc cac gac ctg gtc atc aaa agc ctt gac aaa ttg aag			831
Gln Ala Gln Ala His Asp Leu Val Ile Lys Ser Leu Asp Lys Leu Lys			
240	245	250	
gag gtg aag gag ttt ttg ggt gag aac ata tcc aac ttt ctt tcc tta			879
Glu Val Lys Glu Phe Leu Gly Glu Asn Ile Ser Asn Phe Leu Ser Leu			
255	260	265	
gct ggc aat act tac caa ctc aca cga ggc att ggg aag gac atc cgt			927
Ala Gly Asn Thr Tyr Gln Leu Thr Arg Gly Ile Gly Lys Asp Ile Arg			
270	275	280	
gcc ctc aga cga gcc aga gcc aat ctt cag tca gta ccg cat gcc tca			975
Ala Leu Arg Arg Ala Arg Ala Asn Leu Gln Ser Val Pro His Ala Ser			
285	290	295	300

gcc tca cgc ccc cgg gtc act gag cca atc tca gct gaa agc ggt gaa 1023

Ala Ser Arg Pro Arg Val Thr Glu Pro Ile Ser Ala Glu Ser Gly Glu

305

310

315

cag gtg gag aga gtt aat gaa ccc agc atc ctg gaa atg agc aga gga 1071

Gln Val Glu Arg Val Asn Glu Pro Ser Ile Leu Glu Met Ser Arg Gly

320

325

330

gtc aag ctc acg gat gtg gcc cct gta agc ttc ttt ctt gtg ctg gat 1119

Val Lys Leu Thr Asp Val Ala Pro Val Ser Phe Phe Leu Val Leu Asp

335

340

345

gta gtc tac ctc gtg tac gaa tca aag cac tta cat gag ggg gca aag 1167

Val Val Tyr Leu Val Tyr Glu Ser Lys His Leu His Glu Gly Ala Lys

350

355

360

tca gag aca gct gag gag ctg aag aag gtg gct cag gag ctg gag gag 1215

Ser Glu Thr Ala Glu Glu Leu Lys Lys Val Ala Gln Glu Leu Glu Glu

365

370

375

380

aag cta aac att ctc aac aat aat tat aag att ctg cag gcg gac caa 1263

Lys Leu Asn Ile Leu Asn Asn Asn Tyr Lys Ile Leu Gln Ala Asp Gln

385

390

395

gaa ctg tgaccacagg gcagggcagc caccaggaga gatatgcctg gcaggggccca 1319

Glu Leu

ggacaaaatg caaacitttt tttttctga gacagagtct tgcctgtcg ccaagttgca 1379

gtgagccgag atatgccac tgcactccag cctgggigac agagcgagac tccatclcaa 1439

aaaaaaaaa aaaaagaata tattgacgga agaatagaga ggaggcttga aggaaccagc 1499

aatgagaagg ccaggaaaag aaagagctga aaatggagaa agcccaagag ttagaacagt 1559

tggatacagg agaagaaaca gcggctccac tacagacca gccccaggtt caatgtcttc 1619

cgaagaatga agtctttccc tgggatggg cccctgccct gctttccag catccactct 1679

cccttgctct cctgggggca tatctcagtc aggcagcggc ttctgatga tggtcgttgg 1739

ggtggttgtc atgtgatggg tccccccag gttactaaag ggtgcatgtc ccttgcttga 1799

acactgaagg gcaggtggig agccatggcc atggccccca gctgaggagc aggtgtccct 1859

gagaaccaa acttcccaga gagtatgiga gaaccaacca atgaaaacag tcccatcgct 1919

cttaccgggt aagtaaacag tcagaaaatt agcatgaaag cagtttagca ttgggaggaa 1979

gctcagatct ctagagctgt cttgtccccg cccaggattg acctgtgtaa gtcccataa 2039

actcacctac tcac 2054

<210> 119

<211> 398

<212> PRT

<213> Homo sapiens

<400> 119

Met Glu Gly Ala Ala Leu Leu Arg Val Ser Val Leu Cys Ile Trp Met

1 5 10 15

Ser Ala Leu Phe Leu Gly Val Arg Val Arg Ala Glu Glu Ala Gly Ala

20 25 30

Arg Val Gln Gln Asn Val Pro Ser Gly Thr Asp Thr Gly Asp Pro Gln

35 40 45

Ser Lys Pro Leu Gly Asp Trp Ala Ala Gly Thr Met Asp Pro Glu Ser

50 55 60

Ser Ile Phe Ile Glu Asp Ala Ile Lys Tyr Phe Lys Glu Lys Val Ser

65 70 75 80

Thr Gln Asn Leu Leu Leu Leu Thr Asp Asn Glu Ala Trp Asn Gly

85 90 95

Phe Val Ala Ala Ala Glu Leu Pro Arg Asn Glu Ala Asp Glu Leu Arg

100 105 110

Lys Ala Leu Asp Asn Leu Ala Arg Gln Met Ile Met Lys Asp Lys Asn

115 120 125

Trp His Asp Lys Gly Gln Gln Tyr Arg Asn Trp Phe Leu Lys Glu Phe

130 135 140

Pro Arg Leu Lys Ser Lys Leu Glu Asp Asn Ile Arg Arg Leu Arg Ala
145 150 155 160

Leu Ala Asp Gly Val Gln Lys Val His Lys Gly Thr Thr Ile Ala Asn
165 170 175

Val Val Ser Gly Ser Leu Ser Ile Ser Ser Gly Ile Leu Thr Leu Val
180 185 190

Gly Met Gly Leu Ala Pro Phe Thr Glu Gly Gly Ser Leu Val Leu Leu
195 200 205

Glu Pro Gly Met Glu Leu Gly Ile Thr Ala Ala Leu Thr Gly Ile Thr
210 215 220

Ser Ser Thr Ile Asp Tyr Gly Lys Lys Trp Trp Thr Gln Ala Gln Ala
225 230 235 240

His Asp Leu Val Ile Lys Ser Leu Asp Lys Leu Lys Glu Val Lys Glu
245 250 255

Phe Leu Gly Glu Asn Ile Ser Asn Phe Leu Ser Leu Ala Gly Asn Thr
260 265 270

Tyr Gln Leu Thr Arg Gly Ile Gly Lys Asp Ile Arg Ala Leu Arg Arg
275 280 285

Ala Arg Ala Asn Leu Gln Ser Val Pro His Ala Ser Ala Ser Arg Pro

290

295

300

Arg Val Thr Glu Pro Ile Ser Ala Glu Ser Gly Glu Gln Val Glu Arg

305

310

315

320

Val Asn Glu Pro Ser Ile Leu Glu Met Ser Arg Gly Val Lys Leu Thr

325

330

335

Asp Val Ala Pro Val Ser Phe Phe Leu Val Leu Asp Val Val Tyr Leu

340

345

350

Val Tyr Glu Ser Lys His Leu His Glu Gly Ala Lys Ser Glu Thr Ala

355

360

365

Glu Glu Leu Lys Lys Val Ala Gln Glu Leu Glu Glu Lys Leu Asn Ile

370

375

380

Leu Asn Asn Asn Tyr Lys Ile Leu Gln Ala Asp Gln Glu Leu

385

390

395

<210> 120

<211> 2054

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (76).. (1269)

<400> 120

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aggccctgca gcgac atg gag gga gct gct ttg ctg aga gtc tct gtc ctc 111

Met Glu Gly Ala Ala Leu Leu Arg Val Ser Val Leu

1

5

10

tgc atc tgg atg agt gca ctt ttc ctt ggt gtg aga gtg agg gca gag 159

Cys Ile Trp Met Ser Ala Leu Phe Leu Gly Val Arg Val Arg Ala Glu

15

20

25

gaa gct gga gcg agg gtg caa caa aac gtt cca agt ggg aca gat act 207

Glu Ala Gly Ala Arg Val Gln Gln Asn Val Pro Ser Gly Thr Asp Thr

30

35

40

gga gat cct caa agt aag ccc ctc ggt gac tgg gct gct ggc acc atg 255

Gly Asp Pro Gln Ser Lys Pro Leu Gly Asp Trp Ala Ala Gly Thr Met

45

50

55

60

gac cca gag agc agt atc ttt att gag gat gcc att aag tat ttc aag 303

Asp Pro Glu Ser Ser Ile Phe Ile Glu Asp Ala Ile Lys Tyr Phe Lys

65

70

75

gaa aaa gtg agc aca cag aat ctg cta ctc ctg ctg act gat aat gag 351

Glu Lys Val Ser Thr Gln Asn Leu Leu Leu Leu Leu Thr Asp Asn Glu

80

85

90

gcc tgg aac gga ttc gtg gct gct gct gaa ctg ccc agg aat gag gca 399

Ala Trp Asn Gly Phe Val Ala Ala Ala Glu Leu Pro Arg Asn Glu Ala

95

100

105

gat gag ctc cgt aaa gct ctg gac aac ctt gca aga caa atg atc atg 447

Asp Glu Leu Arg Lys Ala Leu Asp Asn Leu Ala Arg Gln Met Ile Met

110

115

120

aaa gac aaa aac tgg cac gat aaa ggc cag cag tac aga aac tgg ttt 495

Lys Asp Lys Asn Trp His Asp Lys Gly Gln Gln Tyr Arg Asn Trp Phe

125

130

135

140

ctg aaa gag ttt cct cgg ttg aaa agt aag ctt gag gat aac ata aga 543

Leu Lys Glu Phe Pro Arg Leu Lys Ser Lys Leu Glu Asp Asn Ile Arg

145

150

155

agg ctc cgt gcc ctt gca gat ggg gtt cag aag gtc cac aaa ggc acc 591

Arg Leu Arg Ala Leu Ala Asp Gly Val Gln Lys Val His Lys Gly Thr

160

165

170

acc atc gcc aat gtg gtg tct ggc tct ctc agc att tcc tct ggc atc 639

Thr Ile Ala Asn Val Val Ser Gly Ser Leu Ser Ile Ser Ser Gly Ile

175

180

185

ctg acc ctc gtc ggc atg ggt ctg gca ccc ttc aca gag gga ggc agc 687

Leu Thr Leu Val Gly Met Gly Leu Ala Pro Phe Thr Glu Gly Gly Ser

190

195

200

ctt gta ctc ttg gaa cct ggg atg gag ttg gga atc aca gca gct ttg 735

Leu Val Leu Leu Glu Pro Gly Met Glu Leu Gly Ile Thr Ala Ala Leu

205	210	215	220	
acc ggg att acc agc agt acc ata gac tac gga aag aag tgg tgg aca				783
Thr Gly Ile Thr Ser Ser Thr Ile Asp Tyr Gly Lys Lys Trp Trp Thr				
	225	230	235	
caa gcc caa gcc cac gac ctg gtc atc aaa agc ctt gac aaa ttg aag				831
Gln Ala Gln Ala His Asp Leu Val Ile Lys Ser Leu Asp Lys Leu Lys				
	240	245	250	
gag gtg aag gag ttt ttg ggt gag aac ata tcc aac ttt ctt tcc tta				879
Glu Val Lys Glu Phe Leu Gly Glu Asn Ile Ser Asn Phe Leu Ser Leu				
	255	260	265	
gct ggc aat act tac caa ctc aca cga ggc att ggg aag gac atc cgt				927
Ala Gly Asn Thr Tyr Gln Leu Thr Arg Gly Ile Gly Lys Asp Ile Arg				
	270	275	280	
gcc ctc aga cga gcc aga gcc aat ctt cag tca gta ccg cat gcc tca				975
Ala Leu Arg Arg Ala Arg Ala Asn Leu Gln Ser Val Pro His Ala Ser				
285	290	295	300	
gcc tca cgc ccc cgg gtc act gag cca atc tca gct gaa agc ggt gaa				1023
Ala Ser Arg Pro Arg Val Thr Glu Pro Ile Ser Ala Glu Ser Gly Glu				
	305	310	315	
cag gtg gag aga gtt aat gaa ccc agc atc ctg gaa atg agc aga gga				1071
Gln Val Glu Arg Val Asn Glu Pro Ser Ile Leu Glu Met Ser Arg Gly				
	320	325	330	

gtc aag ctc acg gat gtg gcc cct gta agc ttc ttt ctt gtg ctg gat 1119

Val Lys Leu Thr Asp Val Ala Pro Val Ser Phe Phe Leu Val Leu Asp

335

340

345

gta gtc tac ctc gtg tac gaa tca aag cac tta cat gag ggg gca aag 1167

Val Val Tyr Leu Val Tyr Glu Ser Lys His Leu His Glu Gly Ala Lys

350

355

360

tca gag aca gct gag gag ctg aag aag gtg gct cag gag ctg gag gag 1215

Ser Glu Thr Ala Glu Glu Leu Lys Lys Val Ala Gln Glu Leu Glu Glu

365

370

375

380

aag cta aac att ctc aac aat aat tat aag att ctg cag gcg gac caa 1263

Lys Leu Asn Ile Leu Asn Asn Asn Tyr Lys Ile Leu Gln Ala Asp Gln

385

390

395

gaa ctg tgaccacagg gcagggcagc caccaggaga gatatgcctg gcaggggccca 1319

Glu Leu

ggacaaaatg caaacTTTTT ttttttctga gacagagctt tgctctgtcg ccaagttgca 1379

gtgagccgag atatcgccac tgcactccag cctgggtgac agagcgagac tccatctcaa 1439

aaaaaaaaa aaaaagaata tattgacgga agaatagaga ggaggcttga aggaaccagc 1499

aatgagaagg ccaggaaaag aaagagctga aaatggagaa agcccaagag ttagaacagt 1559

tggatacagg agaagaaaca gcggctccac tacagacca gccccaggtt caatgtcctc 1619

cgaagaatga agtctttccc tggatgatgt cccctgccct gtctttccag catccactct 1679

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ggtggttgtc atgtgatggg tccccccag gttactaaag ggtgcatgtc cctgcctga 1799

acactgaagg gcaggtagtg agccatggcc atggccccca gctgaggagc aggtgtccct 1859

gagaacccaa acttcccaga gagtatgtga gaaccaacca atgaaaacag tcccatcgct 1919

cttaccgggt aagtaaacag tcagaaaatt agcatgaaag cagtttagca ttgggaggaa 1979

gtcagatct ctagagctgt cttgtccccg cccaggattg acctgtgtaa gtcccaataa 2039

actcacctac tcac 2054

<210> 121

<211> 108

<212> PRT

<213> Homo sapiens

<400> 121

Met Gly Val Gln Val Glu Thr Ile Ser Pro Gly Asp Gly Arg Thr Phe

1

5

10

15

Pro Lys Arg Gly Gln Thr Cys Val Val His Tyr Thr Gly Met Leu Glu

20

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Asp Gly Lys Lys Phe Asp Ser Ser Arg Asp Arg Asn Lys Pro Phe Lys

35

40

45

Phe Met Leu Gly Lys Gln Glu Val Ile Arg Gly Trp Glu Glu Gly Val

50

55

60

Ala Gln Met Ser Val Gly Gln Arg Ala Lys Leu Thr Ile Ser Pro Asp

65

70

75

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Tyr Ala Tyr Gly Ala Thr Gly His Pro Gly Ile Ile Pro Pro His Ala

85

90

95

Thr Leu Val Phe Asp Val Glu Leu Leu Lys Leu Glu

100

105

<210> 122

<211> 1546

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (89).. (412)

<400> 122

actaggcaga gccgtggaac cgccgccagg tcgctgttgg tccacgccgc ccgtcgcgcc 60

gccccccgc tcagcgtccg ccgcccgc atg gga gtg cag gtg gaa acc atc 112

Met Gly Val Gln Val Glu Thr Ile

1

5

tcc cca gga gac ggg cgc acc ttc ccc aag cgc ggc cag acc tgc gtg 160

Ser Pro Gly Asp Gly Arg Thr Phe Pro Lys Arg Gly Gln Thr Cys Val

10

15

20

gtg cac tac acc ggg atg ctt gaa gat gga aag aaa ttt gat tcc tcc 208

Val His Tyr Thr Gly Met Leu Glu Asp Gly Lys Lys Phe Asp Ser Ser

25

30

35

40

cgg gac aga aac aag ccc ttt aag ttt atg cta ggc aag cag gag gtg 256

Arg Asp Arg Asn Lys Pro Phe Lys Phe Met Leu Gly Lys Gln Glu Val

45

50

55

atc cga ggc tgg gaa gaa ggg gtt gcc cag atg agt gtg ggt cag aga 304

Ile Arg Gly Trp Glu Glu Gly Val Ala Gln Met Ser Val Gly Gln Arg

60

65

70

gcc aaa ctg act ata tct cca gat tat gcc tat ggt gcc act ggg cac 352

Ala Lys Leu Thr Ile Ser Pro Asp Tyr Ala Tyr Gly Ala Thr Gly His

75

80

85

cca ggc atc atc cca cca cat gcc act ctc gtc ttc gat gtg gag ctt 400

Pro Gly Ile Ile Pro Pro His Ala Thr Leu Val Phe Asp Val Glu Leu

90

95

100

cta aaa ctg gaa tgacaggaat ggccctcctcc cttagctccc tgttcttggga 452

Leu Lys Leu Glu

105

tctgccatgg agggatctgg tgcctccaga catgtgcaca tgaatccata tggagctttt 512

cctgatgttc cactccactt tgtatagaca tctgccctga ctgaatgtgt tctgtcactc 572

agctttgctt ccgacacctc tgtttcctct tcccccttct cctcgtatgt gtgtttacct 632

aaactatatg ccataaacct caagttactc attttatitt gtittcattt tggggatgaag 692

attcagtttc agtcttttgg atataggttt ccaattaagt acatgggtcaa gtattaacag 752

cacaagtggg aggttaacat tagaatagga attgggtgtg gggggggggg ttgcaagaat 812

attttatitt aatttttgg atgaaatttt tatctattat atattaaaca ttcttgctgc 872

tgcgtgcaa agccatagca gatttagagg gtgttgagg actgaattac tctccaagtt 932

gagagatgtc tttgggttaa attaaaagcc ctacctaaaa ctgagggtgg gatggggaga 992

gcctttgcct ccaccattcc caccaccct ccccttaaac cctctgcctt tgaaagtaga 1052

tcatgttcac tgcaatgtg gacactacag gtatctgtcc ctgggccagc agggacctct 1112

gaagccttct ttgtggcctt ttttttttt tcatcctgtg gtttttctaa tggactttca 1172

ggaattttgt aatctcataa ctltccaagc tccaccactt cctaaatctt aagaacttta 1232

attgacagtt tcaattgaag gtgctgtttg tagacttaac acccagtgaag agcccagcca 1292

tcatgacaaa tccttgaatg ttctcttaag aaaatgatgc tggcatcgc agcttcagca 1352

ttctctgttt ttgatgctt ggctccctct gctgatctca gtttctggc ttttctccc 1412

tcagccctt ctcacccctt tgctgtcctg tgtagtatt tggtagagaa tcgttgctgc 1472

acccttccc cagcaccatt tatgagctc aagttttatt attgcaataa aagtgcctta 1532

tgccggcttt tctc 1546

<210> 123

<211> 679

<212> PRT

<213> Homo sapiens

<400> 123

Met Ala Thr Leu Ile Thr Ser Thr Thr Ala Ala Thr Ala Ala Ser Gly

1 5 10 15

Pro Leu Val Asp Tyr Leu Trp Met Leu Ile Leu Gly Phe Ile Ile Ala

20 25 30

Phe Val Leu Ala Phe Ser Val Gly Ala Asn Asp Val Ala Asn Ser Phe

35 40 45

Gly Thr Ala Val Gly Ser Gly Val Val Thr Leu Lys Gln Ala Cys Ile

50	55	60
Leu Ala Ser Ile Phe Glu Thr Val Gly Ser Val Leu Leu Gly Ala Lys		
65	70	75
80		
Val Ser Glu Thr Ile Arg Lys Gly Leu Ile Asp Val Glu Met Tyr Asn		
85	90	95
Ser Thr Gln Gly Leu Leu Met Ala Gly Ser Val Ser Ala Met Phe Gly		
100	105	110
Ser Ala Val Trp Gln Leu Val Ala Ser Phe Leu Lys Leu Pro Ile Ser		
115	120	125
Gly Thr His Cys Ile Val Gly Ala Thr Ile Gly Phe Ser Leu Val Ala		
130	135	140
Lys Gly Gln Glu Gly Val Lys Trp Ser Glu Leu Ile Lys Ile Val Met		
145	150	155
160		
Ser Trp Phe Val Ser Pro Leu Leu Ser Gly Ile Met Ser Gly Ile Leu		
165	170	175
Phe Phe Leu Val Arg Ala Phe Ile Leu His Lys Ala Asp Pro Val Pro		
180	185	190
Asn Gly Leu Arg Ala Leu Pro Val Phe Tyr Ala Cys Thr Val Gly Ile		
195	200	205

Asn Leu Phe Ser Ile Met Tyr Thr Gly Ala Pro Leu Leu Gly Phe Asp
210 215 220

Lys Leu Pro Leu Trp Gly Thr Ile Leu Ile Ser Val Gly Cys Ala Val
225 230 235 240

Phe Cys Ala Leu Ile Val Trp Phe Phe Val Cys Pro Arg Met Lys Arg
245 250 255

Lys Ile Glu Arg Glu Ile Lys Cys Ser Pro Ser Glu Ser Pro Leu Met
260 265 270

Glu Lys Lys Asn Ser Leu Lys Glu Asp His Glu Glu Thr Lys Leu Ser
275 280 285

Val Gly Asp Ile Glu Asn Lys His Pro Val Ser Glu Val Gly Pro Ala
290 295 300

Thr Val Pro Leu Gln Ala Val Val Glu Glu Arg Thr Val Ser Phe Lys
305 310 315 320

Leu Gly Asp Leu Glu Glu Ala Pro Glu Arg Glu Arg Leu Pro Ser Val
325 330 335

Asp Leu Lys Glu Glu Thr Ser Ile Asp Ser Thr Val Asn Gly Ala Val
340 345 350

Gln Leu Pro Asn Gly Asn Leu Val Gln Phe Ser Gln Ala Val Ser Asn
355 360 365

Gln Ile Asn Ser Ser Gly His Tyr Gln Tyr His Thr Val His Lys Asp

370

375

380

Ser Gly Leu Tyr Lys Glu Leu Leu His Lys Leu His Leu Ala Lys Val

385

390

395

400

Gly Asp Cys Met Gly Asp Ser Gly Asp Lys Pro Leu Arg Arg Asn Asn

405

410

415

Ser Tyr Thr Ser Tyr Thr Met Ala Ile Cys Gly Met Pro Leu Asp Ser

420

425

430

Phe Arg Ala Lys Glu Gly Glu Gln Lys Gly Glu Glu Met Glu Lys Leu

435

440

445

Thr Trp Pro Asn Ala Asp Ser Lys Lys Arg Ile Arg Met Asp Ser Tyr

450

455

460

Thr Ser Tyr Cys Asn Ala Val Ser Asp Leu His Ser Ala Ser Glu Ile

465

470

475

480

Asp Met Ser Val Lys Ala Glu Met Gly Leu Gly Asp Arg Lys Gly Ser

485

490

495

Asn Gly Ser Leu Glu Glu Trp Tyr Asp Gln Asp Lys Pro Glu Val Ser

500

505

510

Leu Leu Phe Gln Phe Leu Gln Ile Leu Thr Ala Cys Phe Gly Ser Phe

515

520

525

Ala His Gly Gly Asn Asp Val Ser Asn Ala Ile Gly Pro Leu Val Ala

530

535

540

Leu Tyr Leu Val Tyr Asp Thr Gly Asp Val Ser Ser Lys Val Ala Thr

545

550

555

560

Pro Ile Trp Leu Leu Leu Tyr Gly Gly Val Gly Ile Cys Val Gly Leu

565

570

575

Trp Val Trp Gly Arg Arg Val Ile Gln Thr Met Gly Lys Asp Leu Thr

580

585

590

Pro Ile Thr Pro Ser Ser Gly Phe Ser Ile Glu Leu Ala Ser Ala Leu

595

600

605

Thr Val Val Ile Ala Ser Asn Ile Gly Leu Pro Ile Ser Thr Thr His

610

615

620

Cys Lys Val Gly Ser Val Val Ser Val Gly Trp Leu Arg Ser Lys Lys

625

630

635

640

Ala Val Asp Trp Arg Leu Phe Arg Asn Ile Phe Met Ala Trp Phe Val

645

650

655

Thr Val Pro Ile Ser Gly Val Ile Ser Ala Ala Ile Met Ala Ile Phe

660

665

670

Arg Tyr Val Ile Leu Arg Met

675

<210> 124

<211> 2916

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (81).. (2117)

<400> 124

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aacaaccact actccagaga atg gca acg ctg att acc agt act aca gct gct 113

Met Ala Thr Leu Ile Thr Ser Thr Thr Ala Ala

1

5

10

acc gcc gct tct ggt cct ttg gtg gac tac cta tgg atg ctc atc ctg 161

Thr Ala Ala Ser Gly Pro Leu Val Asp Tyr Leu Trp Met Leu Ile Leu

15

20

25

ggc ttc att att gca ttt gtc ttg gca ttc tcc gtg gga gcc aat gat 209

Gly Phe Ile Ile Ala Phe Val Leu Ala Phe Ser Val Gly Ala Asn Asp

30

35

40

gta gca aat tct ttt ggt aca gct gtg ggc tca ggt gta gtg acc ctg 257

Val Ala Asn Ser Phe Gly Thr Ala Val Gly Ser Gly Val Val Thr Leu

45

50

55

aag caa gcc tgc atc cta gct agc atc ttt gaa aca gtg ggc tct gtc 305

Lys Gln Ala Cys Ile Leu Ala Ser Ile Phe Glu Thr Val Gly Ser Val

60

65

70

75

tta ctg ggg gcc aaa gtg agc gaa acc atc cgg aag ggc ttg att gac 353

Leu Leu Gly Ala Lys Val Ser Glu Thr Ile Arg Lys Gly Leu Ile Asp

80

85

90

gtg gag atg tac aac tcg act caa ggg ctg ctg atg gcc ggc tca gtc 401

Val Glu Met Tyr Asn Ser Thr Gln Gly Leu Leu Met Ala Gly Ser Val

95

100

105

agt gct atg ttt ggt tct gct gtg tgg caa ctc gtg gct tcg ttt ttg 449

Ser Ala Met Phe Gly Ser Ala Val Trp Gln Leu Val Ala Ser Phe Leu

110

115

120

aag ctc cct att tct gga acc cat tgt att gtt ggt gca act att ggt 497

Lys Leu Pro Ile Ser Gly Thr His Cys Ile Val Gly Ala Thr Ile Gly

125

130

135

ttc tcc ctc gtg gca aag ggg cag gag ggt gtc aag tgg tct gaa ctg 545

Phe Ser Leu Val Ala Lys Gly Gln Glu Gly Val Lys Trp Ser Glu Leu

140

145

150

155

ata aaa att gtg atg tct tgg ttc gtg tcc cca ctg ctt tct gga att 593

Ile Lys Ile Val Met Ser Trp Phe Val Ser Pro Leu Leu Ser Gly Ile

160	165	170	
atg tct gga att tta ttc ttc ctg gtt cgt gca ttc atc ctc cat aag			641
Met Ser Gly Ile Leu Phe Phe Leu Val Arg Ala Phe Ile Leu His Lys			
175	180	185	
gca gat cca gtt cct aat ggt ttg cga gct ttg cca gtt ttc tat gcc			689
Ala Asp Pro Val Pro Asn Gly Leu Arg Ala Leu Pro Val Phe Tyr Ala			
190	195	200	
tgc aca gtt gga ata aac ctc ttt tcc atc atg tat act gga gca ccg			737
Cys Thr Val Gly Ile Asn Leu Phe Ser Ile Met Tyr Thr Gly Ala Pro			
205	210	215	
ttg ctg ggc ttt gac aaa ctt cct ctg tgg ggt acc atc ctc atc tcg			785
Leu Leu Gly Phe Asp Lys Leu Pro Leu Trp Gly Thr Ile Leu Ile Ser			
220	225	230	235
gtg gga tgt gca gtt ttc tgt gcc ctt atc gtc tgg ttc ttt gta tgt			833
Val Gly Cys Ala Val Phe Cys Ala Leu Ile Val Trp Phe Phe Val Cys			
240	245	250	
ccc agg atg aag aga aaa att gaa cga gaa ata aag tgt agt cct tct			881
Pro Arg Met Lys Arg Lys Ile Glu Arg Glu Ile Lys Cys Ser Pro Ser			
255	260	265	
gaa agc ccc tta atg gaa aaa aag aat agc ttg aaa gaa gac cat gaa			929
Glu Ser Pro Leu Met Glu Lys Lys Asn Ser Leu Lys Glu Asp His Glu			
270	275	280	

gaa aca aag ttg tct gtt ggt gat att gaa aac aag cat cct gtt tct 977

Glu Thr Lys Leu Ser Val Gly Asp Ile Glu Asn Lys His Pro Val Ser

285

290

295

gag gta ggg cct gcc act gtg ccc ctc cag gct gtg gtg gag gag aga 1025

Glu Val Gly Pro Ala Thr Val Pro Leu Gln Ala Val Val Glu Glu Arg

300

305

310

315

aca gtc tca ttc aaa ctt gga gat ttg gag gaa gct cca gag aga gag 1073

Thr Val Ser Phe Lys Leu Gly Asp Leu Glu Glu Ala Pro Glu Arg Glu

320

325

330

agg ctt ccc agc gtg gac ttg aaa gag gaa acc agc ata gat agc acc 1121

Arg Leu Pro Ser Val Asp Leu Lys Glu Glu Thr Ser Ile Asp Ser Thr

335

340

345

gtg aat ggt gca gtg cag ttg cct aat ggg aac ctt gtc cag ttc agt 1169

Val Asn Gly Ala Val Gln Leu Pro Asn Gly Asn Leu Val Gln Phe Ser

350

355

360

caa gcc gtc agc aac caa ata aac tcc agt ggc cac tac cag tat cac 1217

Gln Ala Val Ser Asn Gln Ile Asn Ser Ser Gly His Tyr Gln Tyr His

365

370

375

acc gtg cat aag gat tcc ggc ctg tac aaa gag cta ctc cat aaa tta 1265

Thr Val His Lys Asp Ser Gly Leu Tyr Lys Glu Leu Leu His Lys Leu

380

385

390

395

cat ctt gcc aag gtg gga gat tgc atg gga gac tcc ggt gac aaa ccc 1313
His Leu Ala Lys Val Gly Asp Cys Met Gly Asp Ser Gly Asp Lys Pro
400 405 410

tta agg cgc aat aat agc tat act tcc tat acc atg gca ata tgt ggc 1361
Leu Arg Arg Asn Asn Ser Tyr Thr Ser Tyr Thr Met Ala Ile Cys Gly
415 420 425

atg cct ctg gat tca ttc cgt gcc aaa gaa ggt gaa cag aag ggc gaa 1409
Met Pro Leu Asp Ser Phe Arg Ala Lys Glu Gly Glu Gln Lys Gly Glu
430 435 440

gaa atg gag aag ctg aca tgg cct aat gca gac tcc aag aag cga att 1457
Glu Met Glu Lys Leu Thr Trp Pro Asn Ala Asp Ser Lys Lys Arg Ile
445 450 455

cga atg gac agt tac acc agt tac tgc aat gct gtg tct gac ctt cac 1505
Arg Met Asp Ser Tyr Thr Ser Tyr Cys Asn Ala Val Ser Asp Leu His
460 465 470 475

tca gca tct gag ata gac atg agt gtc aag gca gag atg ggt cta ggt 1553
Ser Ala Ser Glu Ile Asp Met Ser Val Lys Ala Glu Met Gly Leu Gly
480 485 490

gac aga aaa gga agt aat ggc tct cta gaa gaa tgg tat gac cag gat 1601
Asp Arg Lys Gly Ser Asn Gly Ser Leu Glu Glu Trp Tyr Asp Gln Asp
495 500 505

aag cct gaa gtc tct ctc ctc ttc cag ttc ctg cag atc ctt aca gcc 1649

Lys Pro Glu Val Ser Leu Leu Phe Gln Phe Leu Gln Ile Leu Thr Ala
 510 515 520

tgc ttt ggg tca ttc gcc cat ggt ggc aat gac gta agc aat gcc att 1697
 Cys Phe Gly Ser Phe Ala His Gly Gly Asn Asp Val Ser Asn Ala Ile
 525 530 535

ggg cct ctg gtt gct tta tat ttg gtt tat gac aca gga gat gtt tct 1745
 Gly Pro Leu Val Ala Leu Tyr Leu Val Tyr Asp Thr Gly Asp Val Ser
 540 545 550 555

tca aaa gtg gca aca cca ata tgg ctt cta ctc tat ggt ggt gtt ggt 1793
 Ser Lys Val Ala Thr Pro Ile Trp Leu Leu Leu Tyr Gly Gly Val Gly
 560 565 570

atc tgt gtt ggt ctg tgg gtt tgg gga aga aga gtt atc cag acc atg 1841
 Ile Cys Val Gly Leu Trp Val Trp Gly Arg Arg Val Ile Gln Thr Met
 575 580 585

ggg aag gat ctg aca ccg atc aca ccc tct agt ggc ttc agt att gaa 1889
 Gly Lys Asp Leu Thr Pro Ile Thr Pro Ser Ser Gly Phe Ser Ile Glu
 590 595 600

ctg gca tct gcc ctc act gtg gtg att gca tca aat att ggc ctt ccc 1937
 Leu Ala Ser Ala Leu Thr Val Val Ile Ala Ser Asn Ile Gly Leu Pro
 605 610 615

atc agt aca aca cat tgt aaa gtg ggc tct gtt gtg tct gtt ggc tgg 1985
 Ile Ser Thr Thr His Cys Lys Val Gly Ser Val Val Ser Val Gly Trp

620

625

630

635

ctc cgg tcc aag aag gct gtt gac tgg cgt ctc ttt cgt aac att ttt 2033
 Leu Arg Ser Lys Lys Ala Val Asp Trp Arg Leu Phe Arg Asn Ile Phe

640

645

650

atg gcc tgg ttt gtc aca gtc cct att tct gga gtt atc agt gct gcc 2081
 Met Ala Trp Phe Val Thr Val Pro Ile Ser Gly Val Ile Ser Ala Ala

655

660

665

atc atg gca atc ttc aga tat gtc atc ctc aga atg tgaagctgtt 2127
 Ile Met Ala Ile Phe Arg Tyr Val Ile Leu Arg Met

670

675

tgagattaaa atttgtgtca atgtttggga ccattcttagg tattcctgct cccctgaaga 2187

atgattacag tgttaacaga agactgacaa gagtcttttt atttgggagc cagaggaggg 2247

aagtgttact tgtgctataa ctgcttttgt gctaaatag aattgtctca aaattagctg 2307

tgtaaaatag cccgggttcc actggtcct gctgaggtcc cctttccttc tgggctgtga 2367

attcctgtac atatttctct actttttgta tcaggttca attccattat gttttaatgt 2427

tgtctctgaa gatgacttgt gatttttttt tctttttttt aaaccatgaa gagccgtttg 2487

acagagcatg ctctgcgttg ttggtttcac cagcttctgc cctcacatgc acagggattt 2547

aacaacaaaa atataactac aacttccctt gtagtctctt atataagtag agtccttggg 2607

actctgccct cctgtcagta gtggcaggat ctattggcat attcgggagc ttcttagagg 2667

gatgaggttc ttigaacaca gtgaaaattt aaattagtaa cttttttgca agcagtttat 2727

tgactgttat tgctaagaag aagtaagaaa gaaaaagcct gtggcaatc ttggttattt 2787

ctttaagatt tctggcagtg tgggatggat gaatgaagtg gaatgtgaac ttggggcaag 2847

ttaaattggga cagccttcca tgttcatttg tctacctctt aactgaataa aaaagcctac 2907

agtttttag 2916

<210> 125

<211> 288

<212> PRT

<213> Homo sapiens

<400> 125

Met Glu Arg Pro Gln Pro Asp Ser Met Pro Gln Asp Leu Ser Glu Ala

1

5

10

15

Leu Lys Glu Ala Thr Lys Glu Val His Thr Gln Ala Glu Asn Ala Glu

20

25

30

Phe Met Arg Asn Phe Gln Lys Gly Gln Val Thr Arg Asp Gly Phe Lys

35

40

45

Leu Val Met Ala Ser Leu Tyr His Ile Tyr Val Ala Leu Glu Glu Glu
50 55 60

Ile Glu Arg Asn Lys Glu Ser Pro Val Phe Ala Pro Val Tyr Phe Pro
65 70 75 80

Glu Glu Leu His Arg Lys Ala Ala Leu Glu Gln Asp Leu Ala Phe Trp
85 90 95

Tyr Gly Pro Arg Trp Gln Glu Val Ile Pro Tyr Thr Pro Ala Met Gln
100 105 110

Arg Tyr Val Lys Arg Leu His Glu Val Gly Arg Thr Glu Pro Glu Leu
115 120 125

Leu Val Ala His Ala Tyr Thr Arg Tyr Leu Gly Asp Leu Ser Gly Gly
130 135 140

Gln Val Leu Lys Lys Ile Ala Gln Lys Ala Leu Asp Leu Pro Ser Ser
145 150 155 160

Gly Glu Gly Leu Ala Phe Phe Thr Phe Pro Asn Ile Ala Ser Ala Thr
165 170 175

Lys Phe Lys Gln Leu Tyr Arg Ser Arg Met Asn Ser Leu Glu Met Thr
180 185 190

Pro Ala Val Arg Gln Arg Val Ile Glu Glu Ala Lys Thr Ala Phe Leu
195 200 205

Leu Asn Ile Gln Leu Phe Glu Glu Leu Gln Glu Leu Leu Thr His Asp
210 215 220

Thr Lys Asp Gln Ser Pro Ser Arg Ala Pro Gly Leu Arg Gln Arg Ala
225 230 235 240

Ser Asn Lys Val Gln Asp Ser Ala Pro Val Glu Thr Pro Arg Gly Lys
245 250 255

Pro Pro Leu Asn Thr Arg Ser Gln Ala Pro Leu Leu Arg Trp Val Leu
260 265 270

Thr Leu Ser Phe Leu Val Ala Thr Val Ala Val Gly Leu Tyr Ala Met
275 280 285

<210> 126

<211> 1550

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (81).. (944)

<400> 126

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acgagcccag caccggccgg atg gag cgt ccg caa ccc gac agc atg ccc cag 113

Met Glu Arg Pro Gln Pro Asp Ser Met Pro Gln

1

5

10

gat ttg tca gag gcc ctg aag gag gcc acc aag gag gtg cac acc cag 161

Asp Leu Ser Glu Ala Leu Lys Glu Ala Thr Lys Glu Val His Thr Gln

15

20

25

gca gag aat gct gag ttc atg agg aac ttt cag aag ggc cag gtg acc 209

Ala Glu Asn Ala Glu Phe Met Arg Asn Phe Gln Lys Gly Gln Val Thr

30

35

40

cga gac ggc ttc aag ctg gtg atg gcc tcc ctg tac cac atc tat gtg 257

Arg Asp Gly Phe Lys Leu Val Met Ala Ser Leu Tyr His Ile Tyr Val

45

50

55

gcc ctg gag gag gag att gag cgc aac aag gag agc cca gtc ttc gcc 305

Ala Leu Glu Glu Glu Ile Glu Arg Asn Lys Glu Ser Pro Val Phe Ala

60

65

70

75

cct gtc tac ttc cca gaa gag ctg cac cgc aag gct gcc ctg gag cag 353

Pro Val Tyr Phe Pro Glu Glu Leu His Arg Lys Ala Ala Leu Glu Gln

80

85

90

gac ctg gcc ttc tgg tac ggg ccc cgc tgg cag gag gtc atc ccc tac 401

Asp Leu Ala Phe Trp Tyr Gly Pro Arg Trp Gln Glu Val Ile Pro Tyr

95

100

105

aca cca gcc atg cag cgc tat gtg aag cgg ctc cac gag gtg ggg cgc 449

Thr Pro Ala Met Gln Arg Tyr Val Lys Arg Leu His Glu Val Gly Arg

110

115

120

aca gag ccc gag ctg ctg gtg gcc cac gcc tac acc cgc tac ctg ggt 497

Thr Glu Pro Glu Leu Leu Val Ala His Ala Tyr Thr Arg Tyr Leu Gly

125

130

135

gac ctg tct ggg ggc cag gtg ctc aaa aag att gcc cag aaa gcc ctg 545

Asp Leu Ser Gly Gly Gln Val Leu Lys Lys Ile Ala Gln Lys Ala Leu

140

145

150

155

gac ctg ccc agc tct ggc gag ggc ctg gcc ttc ttc acc ttc ccc aac 593

Asp Leu Pro Ser Ser Gly Glu Gly Leu Ala Phe Phe Thr Phe Pro Asn

160

165

170

att gcc agt gcc acc aag ttc aag cag ctc tac cgc tcc cgc atg aac 641

Ile Ala Ser Ala Thr Lys Phe Lys Gln Leu Tyr Arg Ser Arg Met Asn

175

180

185

tcc ctg gag atg act ccc gca gtc agg cag agg gtg ata gaa gag gcc 689

Ser Leu Glu Met Thr Pro Ala Val Arg Gln Arg Val Ile Glu Glu Ala

190

195

200

aag act gcg ttc ctg ctc aac atc cag ctc ttt gag gag ttg cag gag 737

Lys Thr Ala Phe Leu Leu Asn Ile Gln Leu Phe Glu Glu Leu Gln Glu

205

210

215

ctg ctg acc cat gac acc aag gac cag agc ccc tca cgg gca cca ggg 785

Leu Leu Thr His Asp Thr Lys Asp Gln Ser Pro Ser Arg Ala Pro Gly

220

225

230

235

ctt cgc cag cgg gcc agc aac aaa gtg caa gat tct gcc ccc gtg gag 833

Leu Arg Gln Arg Ala Ser Asn Lys Val Gln Asp Ser Ala Pro Val Glu

240

245

250

act ccc aga ggg aag ccc cca ctc aac acc cgc tcc cag gct ccg ctt 881

Thr Pro Arg Gly Lys Pro Pro Leu Asn Thr Arg Ser Gln Ala Pro Leu

255

260

265

ctc cga tgg gtc ctt aca ctc agc ttt ctg gtg gcg aca gtt gct gta 929

Leu Arg Trp Val Leu Thr Leu Ser Phe Leu Val Ala Thr Val Ala Val

270

275

280

ggg ctt tat gcc atg tgaatgcagg catgctggct cccagggcca tgaactttgt 984

Gly Leu Tyr Ala Met

285

ccggtggaag gccttccttc tagagaggga attctcttgg ctggttccct taccgtgggc 1044

actgaaggct ttcaggccct ccagccctct cactgtgtcc ctctctcigg aaaggaggaa 1104

ggagcctatg gcatcttccc caacgaaaag cacatccagg caatggccta aatttcagag 1164

ggggcgaagg ggtcagccct gcccttcagc atcctcagtt cctgcagcag agcctggaag 1224

acacccta atgtggcagctg tctcaaacct ccaaaagccc tgagtttcaa giatccttgt 1284

tgacacggcc atgaccactt tccccgtggg ccatggcaat tttacacaa acctgaaaag 1344

atgttgtgtc ttgtgttttt gtcttatttt tgttggagcc actctgttcc tggctcagcc 1404

tcaaatgcag tatttttgtt gtgttctgtt gtttttatag cagggttggg gtggtttttg 1464

agccatgcgt gggtagggag ggagggtgtt aacggcactg tggccttggt ctaacttttg 1524

tgtgaaataa taaacaacat tgtctg 1550

<210> 127

<211> 135

<212> PRT

<213> Homo sapiens

<400> 127

Met Ala Cys Gly Leu Val Ala Ser Asn Leu Asn Leu Lys Pro Gly Glu

1

5

10

15

Cys Leu Arg Val Arg Gly Glu Val Ala Pro Asp Ala Lys Ser Phe Val

20

25

30

Leu Asn Leu Gly Lys Asp Ser Asn Asn Leu Cys Leu His Phe Asn Pro

35

40

45

Arg Phe Asn Ala His Gly Asp Ala Asn Thr Ile Val Cys Asn Ser Lys

50

55

60

Asp Gly Gly Ala Trp Gly Thr Glu Gln Arg Glu Ala Val Phe Pro Phe

65

70

75

80

Gln Pro Gly Ser Val Ala Glu Val Cys Ile Thr Phe Asp Gln Ala Asn

85

90

95

Leu Thr Val Lys Leu Pro Asp Gly Tyr Glu Phe Lys Phe Pro Asn Arg

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Leu Asn Leu Glu Ala Ile Asn Tyr Met Ala Ala Asp Gly Asp Phe Lys

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Ile Lys Cys Val Ala Phe Asp

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<213> Homo sapiens

<220>

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<222> (50).. (454)

<400> 128

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 Gly Leu Val Ala Ser Asn Leu Asn Leu Lys Pro Gly Glu Cys Leu Arg
 5 10 15

gtg cga ggc gag gtg gct cct gac gct aag agc ttc gtg ctg aac ctg 154
 Val Arg Gly Glu Val Ala Pro Asp Ala Lys Ser Phe Val Leu Asn Leu
 20 25 30 35

ggc aaa gac agc aac aac ctg tgc ctg cac ttc aac cct cgc ttc aac 202
 Gly Lys Asp Ser Asn Asn Leu Cys Leu His Phe Asn Pro Arg Phe Asn
 40 45 50

gcc cac ggc gac gcc aac acc atc gtg tgc aac agc aag gac ggc ggc 250
 Ala His Gly Asp Ala Asn Thr Ile Val Cys Asn Ser Lys Asp Gly Gly
 55 60 65

gcc tgg ggg acc gag cag cgg gag gct gtc ttt ccc ttc cag cct gga 298
 Ala Trp Gly Thr Glu Gln Arg Glu Ala Val Phe Pro Phe Gln Pro Gly
 70 75 80

agt gtt gca gag gtg tgc atc acc ttc gac cag gcc aac ctg acc gtc 346
 Ser Val Ala Glu Val Cys Ile Thr Phe Asp Gln Ala Asn Leu Thr Val
 85 90 95

aag ctg cca gat gga tac gaa ttc aag ttc ccc aac cgc ctc aac ctg 394
 Lys Leu Pro Asp Gly Tyr Glu Phe Lys Phe Pro Asn Arg Leu Asn Leu
 100 105 110 115

gag gcc atc aac tac atg gca gct gac ggt gac ttc aag atc aaa tgt 442

Glu Ala Ile Asn Tyr Met Ala Ala Asp Gly Asp Phe Lys Ile Lys Cys

120

125

130

gtg gcc ttt gac tgaaatcagc cagcccatgg cccccaataa aggcagctgc 494

Val Ala Phe Asp

135

ctctgctccc ctg

507

<210> 129

<211> 662

<212> PRT

<213> Homo sapiens

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25

30

Asn Phe Thr Phe Glu Phe Ser Gln Trp Ser Gln Leu Asp Val Cys Asp

35

40

45

Ile Pro Glu Ser Phe Gln Arg Ser Val Asp Gly Val Ser Glu Ser Lys

50

55

60

Leu Gln Ile Cys Val Glu Pro Thr Ser Gln Lys Leu Met Pro Gly Ser

65 70 75 80

Thr Leu Val Leu Gln Cys Val Ala Val Gly Ser Pro Ile Pro His Tyr

85 90 95

Gln Trp Phe Lys Asn Glu Leu Pro Leu Thr His Glu Thr Lys Lys Leu

100 105 110

Tyr Met Val Pro Tyr Val Asp Leu Glu His Gln Gly Thr Tyr Trp Cys

115 120 125

His Val Tyr Asn Asp Arg Asp Ser Gln Asp Ser Lys Lys Val Glu Ile

130 135 140

Ile Ile Gly Arg Thr Asp Glu Ala Val Glu Cys Thr Glu Asp Glu Leu

145 150 155 160

Asn Asn Leu Gly His Pro Asp Asn Lys Glu Gln Thr Thr Asp Gln Pro

165 170 175

Leu Ala Lys Asp Lys Val Ala Leu Leu Ile Gly Asn Met Asn Tyr Arg

180 185 190

Glu His Pro Lys Leu Lys Ala Pro Leu Val Asp Val Tyr Glu Leu Thr

195 200 205

Asn Leu Leu Arg Gln Leu Asp Phe Lys Val Val Ser Leu Leu Asp Leu

210 215 220

Thr Glu Tyr Glu Met Arg Asn Ala Val Asp Glu Phe Leu Leu Leu Leu

225 230 235 240

Asp Lys Gly Val Tyr Gly Leu Leu Tyr Tyr Ala Gly His Gly Tyr Glu

245 250 255

Asn Phe Gly Asn Ser Phe Met Val Pro Val Asp Ala Pro Asn Pro Tyr

260 265 270

Arg Ser Glu Asn Cys Leu Cys Val Gln Asn Ile Leu Lys Leu Met Gln

275 280 285

Glu Lys Glu Thr Gly Leu Asn Val Phe Leu Leu Asp Met Cys Arg Lys

290 295 300

Arg Asn Asp Tyr Asp Asp Thr Ile Pro Ile Leu Asp Ala Leu Lys Val

305 310 315 320

Thr Ala Asn Ile Val Phe Gly Tyr Ala Thr Cys Gln Gly Ala Glu Ala

325 330 335

Phe Glu Ile Gln His Ser Gly Leu Ala Asn Gly Ile Phe Met Lys Phe

340 345 350

Leu Lys Asp Arg Leu Leu Glu Asp Lys Lys Ile Thr Val Leu Leu Asp

355 360 365

Glu Val Ala Glu Asp Met Gly Lys Cys His Leu Thr Lys Gly Lys Gln

370 375 380

Ala Leu Glu Ile Arg Ser Ser Leu Ser Glu Lys Arg Ala Leu Thr Asp

385 390 395 400

Pro Ile Gln Gly Thr Glu Tyr Ser Ala Glu Ser Leu Val Arg Asn Leu

405 410 415

Gln Trp Ala Lys Ala His Glu Leu Pro Glu Ser Met Cys Leu Lys Phe

420 425 430

Asp Cys Gly Val Gln Ile Gln Leu Gly Phe Ala Ala Glu Phe Ser Asn

435 440 445

Val Met Ile Ile Tyr Thr Ser Ile Val Tyr Lys Pro Pro Glu Ile Ile

450 455 460

Met Cys Asp Ala Tyr Val Thr Asp Phe Pro Leu Asp Leu Asp Ile Asp

465 470 475 480

Pro Lys Asp Ala Asn Lys Gly Thr Pro Glu Glu Thr Gly Ser Tyr Leu

485 490 495

Val Ser Lys Asp Leu Pro Lys His Cys Leu Tyr Thr Arg Leu Ser Ser

500 505 510

Leu Gln Lys Leu Lys Glu His Leu Val Phe Thr Val Cys Leu Ser Tyr

515 520 525

Gln Tyr Ser Gly Leu Glu Asp Thr Val Glu Asp Lys Gln Glu Val Asn

530

535

540

Val Gly Lys Pro Leu Ile Ala Lys Leu Asp Met His Arg Gly Leu Gly

545

550

555

560

Arg Lys Thr Cys Phe Gln Thr Cys Leu Met Ser Asn Gly Pro Tyr Gln

565

570

575

Ser Ser Ala Ala Thr Ser Gly Gly Ala Gly His Tyr His Ser Leu Gln

580

585

590

Asp Pro Phe His Gly Val Tyr His Ser His Pro Gly Asn Pro Ser Asn

595

600

605

Val Thr Pro Ala Asp Ser Cys His Cys Ser Arg Thr Pro Asp Ala Phe

610

615

620

Ile Ser Ser Phe Ala His His Ala Ser Cys His Phe Ser Arg Ser Asn

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Val Pro Val Glu Thr Thr Asp Glu Ile Pro Phe Ser Phe Ser Asp Arg

645

650

655

Leu Arg Ile Ser Glu Lys

660

<210> 130

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<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (74).. (2059)

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Met Asn Lys Glu Ile Pro Asn Gly Asn Thr Ser Glu

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10

ctt att ttt aat gca gtg cat gta aaa gat gca ggc ttt tat gtc tgt 157

Leu Ile Phe Asn Ala Val His Val Lys Asp Ala Gly Phe Tyr Val Cys

15

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25

cga gtt aat aac aat ttc acc ttt gaa ttc agc cag tgg tca cag ctg 205

Arg Val Asn Asn Asn Phe Thr Phe Glu Phe Ser Gln Trp Ser Gln Leu

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35

40

gat gtt tgc gac atc cca gag agc ttc cag aga agt gtt gat ggc gtc 253

Asp Val Cys Asp Ile Pro Glu Ser Phe Gln Arg Ser Val Asp Gly Val

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55

60

tct gaa tcc aag ttg caa atc tgt gtt gaa cca act tcc caa aag ctg 301

Ser Glu Ser Lys Leu Gln Ile Cys Val Glu Pro Thr Ser Gln Lys Leu

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70

75

atg cca ggc agc aca ttg gtt tta cag tgt gtt gct gtt gga agc cct 349
 Met Pro Gly Ser Thr Leu Val Leu Gln Cys Val Ala Val Gly Ser Pro
 80 85 90

att cct cac tac cag tgg ttc aaa aat gaa tta cca tta aca cat gag 397
 Ile Pro His Tyr Gln Trp Phe Lys Asn Glu Leu Pro Leu Thr His Glu
 95 100 105

acc aaa aag cta tac atg gtg cct tat gtg gat ttg gaa cac caa gga 445
 Thr Lys Lys Leu Tyr Met Val Pro Tyr Val Asp Leu Glu His Gln Gly
 110 115 120

acc tac tgg tgt cat gta tat aat gat cga gac agt caa gat agc aag 493
 Thr Tyr Trp Cys His Val Tyr Asn Asp Arg Asp Ser Gln Asp Ser Lys
 125 130 135 140

aag gta gaa atc atc ata gga aga aca gat gag gca gtg gag tgc act 541
 Lys Val Glu Ile Ile Ile Gly Arg Thr Asp Glu Ala Val Glu Cys Thr
 145 150 155

gaa gat gaa tta aat aat ctt ggt cat cct gat aat aaa gag caa aca 589
 Glu Asp Glu Leu Asn Asn Leu Gly His Pro Asp Asn Lys Glu Gln Thr
 160 165 170

act gac cag cct ttg gcg aag gac aag gtt gcc ctt ttg ata gga aat 637
 Thr Asp Gln Pro Leu Ala Lys Asp Lys Val Ala Leu Leu Ile Gly Asn
 175 180 185

atg aat tac cgg gag cac ccc aag ctc aaa gct cct ttg gtg gat gtg 685

Met Asn Tyr Arg Glu His Pro Lys Leu Lys Ala Pro Leu Val Asp Val

190

195

200

tac gaa ttg act aac tta ctg aga cag ctg gac ttc aaa gtg gtt tca 733

Tyr Glu Leu Thr Asn Leu Leu Arg Gln Leu Asp Phe Lys Val Val Ser

205

210

215

220

ctg ttg gat ctt act gaa tat gag atg cgt aat gct gtg gat gag ttt 781

Leu Leu Asp Leu Thr Glu Tyr Glu Met Arg Asn Ala Val Asp Glu Phe

225

230

235

tta ctc ctt tta gac aag gga gta tat ggg tta tta tat tat gca gga 829

Leu Leu Leu Leu Asp Lys Gly Val Tyr Gly Leu Leu Tyr Tyr Ala Gly

240

245

250

cat ggt tat gaa aat ttt ggg aac agc ttc atg gtc ccc gtt gat gct 877

His Gly Tyr Glu Asn Phe Gly Asn Ser Phe Met Val Pro Val Asp Ala

255

260

265

cca aat cca tat agg tct gaa aat tgt ctg tgt gta caa aat ata ctg 925

Pro Asn Pro Tyr Arg Ser Glu Asn Cys Leu Cys Val Gln Asn Ile Leu

270

275

280

aaa ttg atg caa gaa aaa gaa act gga ctt aat gtg ttc tta ttg gat 973

Lys Leu Met Gln Glu Lys Glu Thr Gly Leu Asn Val Phe Leu Leu Asp

285

290

295

300

atg tgt agg aaa aga aat gac tac gat gat acc att cca atc ttg gat 1021

Met Cys Arg Lys Arg Asn Asp Tyr Asp Asp Thr Ile Pro Ile Leu Asp
 305 310 315

gca cta aaa gtc acc gcc aat att gtg ttt gga tat gcc acg tgt caa 1069
 Ala Leu Lys Val Thr Ala Asn Ile Val Phe Gly Tyr Ala Thr Cys Gln
 320 325 330

gga gca gaa gct ttt gaa atc cag cat tct gga ttg gca aat gga atc 1117
 Gly Ala Glu Ala Phe Glu Ile Gln His Ser Gly Leu Ala Asn Gly Ile
 335 340 345

ttt atg aaa ttt tta aaa gac aga tta tta gaa gat aag aaa atc act 1165
 Phe Met Lys Phe Leu Lys Asp Arg Leu Leu Glu Asp Lys Lys Ile Thr
 350 355 360

gtg tta ctg gat gaa gtt gca gaa gat atg ggt aag tgt cac ctt acc 1213
 Val Leu Leu Asp Glu Val Ala Glu Asp Met Gly Lys Cys His Leu Thr
 365 370 375 380

aaa ggc aaa cag gct cta gag att cga agt agt tta tct gag aag aga 1261
 Lys Gly Lys Gln Ala Leu Glu Ile Arg Ser Ser Leu Ser Glu Lys Arg
 385 390 395

gca ctt act gat cca ata cag gga aca gaa tat tct gct gaa tct ctt 1309
 Ala Leu Thr Asp Pro Ile Gln Gly Thr Glu Tyr Ser Ala Glu Ser Leu
 400 405 410

gtg cgg aat cta cag tgg gcc aag gct cat gaa ctt cca gaa agt atg 1357
 Val Arg Asn Leu Gln Trp Ala Lys Ala His Glu Leu Pro Glu Ser Met

415	420	425	
tgt ctt aag ttt gac tgt ggt gtt cag att caa tta gga ttt gca gct 1405			
Cys Leu Lys Phe Asp Cys Gly Val Gln Ile Gln Leu Gly Phe Ala Ala			
430	435	440	
gag ttt tcc aat gtc atg atc atc tat aca agt ata gtt tac aaa cca 1453			
Glu Phe Ser Asn Val Met Ile Ile Tyr Thr Ser Ile Val Tyr Lys Pro			
445	450	455	460
ccg gag ata ata atg tgt gat gcc tac gtt act gat ttt cca ctt gat 1501			
Pro Glu Ile Ile Met Cys Asp Ala Tyr Val Thr Asp Phe Pro Leu Asp			
465	470	475	
cta gat att gat cca aaa gat gca aat aaa ggc aca cct gaa gaa act 1549			
Leu Asp Ile Asp Pro Lys Asp Ala Asn Lys Gly Thr Pro Glu Glu Thr			
480	485	490	
ggc agc tac ttg gta tca aag gat ctt ccc aag cat tgc ctc tat acc 1597			
Gly Ser Tyr Leu Val Ser Lys Asp Leu Pro Lys His Cys Leu Tyr Thr			
495	500	505	
aga ctc agt tca ctg caa aaa tta aag gaa cat cta gtc ttc aca gta 1645			
Arg Leu Ser Ser Leu Gln Lys Leu Lys Glu His Leu Val Phe Thr Val			
510	515	520	
tgt tta tca tat cag tac tca gga ttg gaa gat act gta gag gac aag 1693			
Cys Leu Ser Tyr Gln Tyr Ser Gly Leu Glu Asp Thr Val Glu Asp Lys			
525	530	535	540

cag gaa gtg aat gtt ggg aaa cct ctc att gct aaa tta gac atg cat 1741

Gln Glu Val Asn Val Gly Lys Pro Leu Ile Ala Lys Leu Asp Met His

545

550

555

cga ggt ttg gga agg aag act tgc ttt caa act tgt ctt atg tct aat 1789

Arg Gly Leu Gly Arg Lys Thr Cys Phe Gln Thr Cys Leu Met Ser Asn

560

565

570

ggc cct tac cag agt tct gca gcc acc tca gga gga gca ggg cat tat 1837

Gly Pro Tyr Gln Ser Ser Ala Ala Thr Ser Gly Gly Ala Gly His Tyr

575

580

585

cac tca ttg caa gac cca ttc cat ggt gtt tac cat tca cat cct ggt 1885

His Ser Leu Gln Asp Pro Phe His Gly Val Tyr His Ser His Pro Gly

590

595

600

aat cca agt aat gtt aca cca gca gat agc tgt cat tgc agc cgg act 1933

Asn Pro Ser Asn Val Thr Pro Ala Asp Ser Cys His Cys Ser Arg Thr

605

610

615

620

cca gat gca ttt att tca agt ttc gct cac cat gct tca tgt cat ttt 1981

Pro Asp Ala Phe Ile Ser Ser Phe Ala His His Ala Ser Cys His Phe

625

630

635

agt aga agt aat gtg cca gta gag aca act gat gaa ata cca ttt agt 2029

Ser Arg Ser Asn Val Pro Val Glu Thr Thr Asp Glu Ile Pro Phe Ser

640

645

650

ttc tct gac agg ctc aga att tct gaa aaa tgacctcctt gtttttgaaa 2079

Phe Ser Asp Arg Leu Arg Ile Ser Glu Lys

655

660

gttagcataa ttttagatgc ctgtgaaata gtactgcact tacataaagt gagacattgt 2139

gaaaaggcaa atttgtatat gtagagaaag aatagtagta actgtttcat agcaaacttc 2199

aggactttga gatgttgaaa ttacattatt taattacaga cttcctcttt ct - 2251

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<211> 824

<212> PRT

<213> Homo sapiens

<400> 131

Met Ser Leu Leu Gly Asp Pro Leu Gln Ala Leu Pro Pro Ser Ala Ala

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Pro Thr Gly Pro Leu Leu Ala Pro Pro Ala Gly Ala Thr Leu Asn Arg

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25

30

Leu Arg Glu Pro Leu Leu Arg Arg Leu Ser Glu Leu Leu Asp Gln Ala

35

40

45

Pro Glu Gly Arg Gly Trp Arg Arg Leu Ala Glu Leu Ala Gly Ser Arg

50

55

60

Gly Arg Leu Arg Leu Ser Cys Leu Asp Leu Glu Gln Cys Ser Leu Lys
65 70 75 80

Val Leu Glu Pro Glu Gly Ser Pro Ser Leu Cys Leu Leu Lys Leu Met
85 90 95

Gly Glu Lys Gly Cys Thr Val Thr Glu Leu Ser Asp Phe Leu Gln Ala
100 105 110

Met Glu His Thr Glu Val Leu Gln Leu Leu Ser Pro Pro Gly Ile Lys
115 120 125

Ile Thr Val Asn Pro Glu Ser Lys Ala Val Leu Ala Gly Gln Phe Val
130 135 140

Lys Leu Cys Cys Arg Ala Thr Gly His Pro Phe Val Gln Tyr Gln Trp
145 150 155 160

Phe Lys Met Asn Lys Glu Ile Pro Asn Gly Asn Thr Ser Glu Leu Ile
165 170 175

Phe Asn Ala Val His Val Lys Asp Ala Gly Phe Tyr Val Cys Arg Val
180 185 190

Asn Asn Asn Phe Thr Phe Glu Phe Ser Gln Trp Ser Gln Leu Asp Val
195 200 205

Cys Asp Ile Pro Glu Ser Phe Gln Arg Ser Val Asp Gly Val Ser Glu
210 215 220

Ser Lys Leu Gln Ile Cys Val Glu Pro Thr Ser Gln Lys Leu Met Pro
225 230 235 240

Gly Ser Thr Leu Val Leu Gln Cys Val Ala Val Gly Ser Pro Ile Pro
245 250 255

His Tyr Gln Trp Phe Lys Asn Glu Leu Pro Leu Thr His Glu Thr Lys
260 265 270

Lys Leu Tyr Met Val Pro Tyr Val Asp Leu Glu His Gln Gly Thr Tyr
275 280 285

Trp Cys His Val Tyr Asn Asp Arg Asp Ser Gln Asp Ser Lys Lys Val
290 295 300

Glu Ile Ile Ile Gly Arg Thr Asp Glu Ala Val Glu Cys Thr Glu Asp
305 310 315 320

Glu Leu Asn Asn Leu Gly His Pro Asp Asn Lys Glu Gln Thr Thr Asp
325 330 335

Gln Pro Leu Ala Lys Asp Lys Val Ala Leu Leu Ile Gly Asn Met Asn
340 345 350

Tyr Arg Glu His Pro Lys Leu Lys Ala Pro Leu Val Asp Val Tyr Glu
355 360 365

Leu Thr Asn Leu Leu Arg Gln Leu Asp Phe Lys Val Val Ser Leu Leu

370

375

380

Asp Leu Thr Glu Tyr Glu Met Arg Asn Ala Val Asp Glu Phe Leu Leu

385

390

395

400

Leu Leu Asp Lys Gly Val Tyr Gly Leu Leu Tyr Tyr Ala Gly His Gly

405

410

415

Tyr Glu Asn Phe Gly Asn Ser Phe Met Val Pro Val Asp Ala Pro Asn

420

425

430

Pro Tyr Arg Ser Glu Asn Cys Leu Cys Val Gln Asn Ile Leu Lys Leu

435

440

445

Met Gln Glu Lys Glu Thr Gly Leu Asn Val Phe Leu Leu Asp Met Cys

450

455

460

Arg Lys Arg Asn Asp Tyr Asp Asp Thr Ile Pro Ile Leu Asp Ala Leu

465

470

475

480

Lys Val Thr Ala Asn Ile Val Phe Gly Tyr Ala Thr Cys Gln Gly Ala

485

490

495

Glu Ala Phe Glu Ile Gln His Ser Gly Leu Ala Asn Gly Ile Phe Met

500

505

510

Lys Phe Leu Lys Asp Arg Leu Leu Glu Asp Lys Lys Ile Thr Val Leu

515

520

525

Leu Asp Glu Val Ala Glu Asp Met Gly Lys Cys His Leu Thr Lys Gly
530 535 540

Lys Gln Ala Leu Glu Ile Arg Ser Ser Leu Ser Glu Lys Arg Ala Leu
545 550 555 560

Thr Asp Pro Ile Gln Gly Thr Glu Tyr Ser Ala Glu Ser Leu Val Arg
565 570 575

Asn Leu Gln Trp Ala Lys Ala His Glu Leu Pro Glu Ser Met Cys Leu
580 585 590

Lys Phe Asp Cys Gly Val Gln Ile Gln Leu Gly Phe Ala Ala Glu Phe
595 600 605

Ser Asn Val Met Ile Ile Tyr Thr Ser Ile Val Tyr Lys Pro Pro Glu
610 615 620

Ile Ile Met Cys Asp Ala Tyr Val Thr Asp Phe Pro Leu Asp Leu Asp
625 630 635 640

Ile Asp Pro Lys Asp Ala Asn Lys Gly Thr Pro Glu Glu Thr Gly Ser
645 650 655

Tyr Leu Val Ser Lys Asp Leu Pro Lys His Cys Leu Tyr Thr Arg Leu
660 665 670

Ser Ser Leu Gln Lys Leu Lys Glu His Leu Val Phe Thr Val Cys Leu
675 680 685

Ser Tyr Gln Tyr Ser Gly Leu Glu Asp Thr Val Glu Asp Lys Gln Glu
690 695 700

Val Asn Val Gly Lys Pro Leu Ile Ala Lys Leu Asp Met His Arg Gly
705 710 715 720

Leu Gly Arg Lys Thr Cys Phe Gln Thr Cys Leu Met Ser Asn Gly Pro
725 730 735

Tyr Gln Ser Ser Ala Ala Thr Ser Gly Gly Ala Gly His Tyr His Ser
740 745 750

Leu Gln Asp Pro Phe His Gly Val Tyr His Ser His Pro Gly Asn Pro
755 760 765

Ser Asn Val Thr Pro Ala Asp Ser Cys His Cys Ser Arg Thr Pro Asp
770 775 780

Ala Phe Ile Ser Ser Phe Ala His His Ala Ser Cys His Phe Ser Arg
785 790 795 800

Ser Asn Val Pro Val Glu Thr Thr Asp Glu Ile Pro Phe Ser Phe Ser
805 810 815

Asp Arg Leu Arg Ile Ser Glu Lys
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<210> 132

<211> 2828

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

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gggcgggcgg gagccccggc agtccgggggt cgccggcgag ggcc atg tcg ctg ttg 176

Met Ser Leu Leu

1

ggg gac ccg cta cag gcc ctg ccg ccc tcg gcc gcc ccc acg ggg ccg 224

Gly Asp Pro Leu Gln Ala Leu Pro Pro Ser Ala Ala Pro Thr Gly Pro

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10

15

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ctg ctc gcc cct ccg gcc ggc ggc acc ctc aac cgc ctg cgg gag ccg 272

Leu Leu Ala Pro Pro Ala Gly Ala Thr Leu Asn Arg Leu Arg Glu Pro

25

30

35

ctg ctg cgg agg ctc agc gag ctc ctg gat cag gcg ccc gag ggc ccg 320

Leu Leu Arg Arg Leu Ser Glu Leu Leu Asp Gln Ala Pro Glu Gly Arg

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45

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ggc tgg agg aga ctg gcg gag ctg gcg ggg agt cgc ggg cgc ctc cgc 368

Gly Trp Arg Arg Leu Ala Glu Leu Ala Gly Ser Arg Gly Arg Leu Arg

55

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65

ctc agt tgc cta gac ctg gag cag tgt tct ctt aag gta ctg gag cct 416

Leu Ser Cys Leu Asp Leu Glu Gln Cys Ser Leu Lys Val Leu Glu Pro

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75

80

gaa gga agc ccc agc ctg tgt ctg ctg aag tta atg ggt gaa aaa ggt 464

Glu Gly Ser Pro Ser Leu Cys Leu Leu Lys Leu Met Gly Glu Lys Gly

85

90

95

100

tgc aca gtc aca gaa ttg agt gat ttc ctg cag gct atg gaa cac act 512

Cys Thr Val Thr Glu Leu Ser Asp Phe Leu Gln Ala Met Glu His Thr

105

110

115

gaa gtt ctt cag ctt ctc agc ccc cca gga ata aag att act gta aac 560

Glu Val Leu Gln Leu Leu Ser Pro Pro Gly Ile Lys Ile Thr Val Asn

120

125

130

cca gag tca aag gca gtc ttg gct gga cag ttt gtg aaa ctg tgt tgc 608

Pro Glu Ser Lys Ala Val Leu Ala Gly Gln Phe Val Lys Leu Cys Cys

135

140

145

cgg gca act gga cat cct ttt gtt caa tat cag tgg ttc aaa atg aat 656

Arg Ala Thr Gly His Pro Phe Val Gln Tyr Gln Trp Phe Lys Met Asn

150

155

160

aaa gag att cca aat gga aat aca tca gag ctt att ttt aat gca gtg 704

Lys Glu Ile Pro Asn Gly Asn Thr Ser Glu Leu Ile Phe Asn Ala Val

165

170

175

180

cat gta aaa gat gca ggc ttt tat gtc tgt cga gtt aat aac aat ttc 752

His Val Lys Asp Ala Gly Phe Tyr Val Cys Arg Val Asn Asn Asn Phe

185

190

195

acc ttt gaa ttc agc cag tgg tca cag ctg gat gtt tgc gac atc cca 800

Thr Phe Glu Phe Ser Gln Trp Ser Gln Leu Asp Val Cys Asp Ile Pro

200

205

210

gag agc ttc cag aga agt gtt gat ggc gtc tct gaa tcc aag ttg caa 848

Glu Ser Phe Gln Arg Ser Val Asp Gly Val Ser Glu Ser Lys Leu Gln

215

220

225

atc tgt gtt gaa cca act tcc caa aag ctg atg cca ggc agc aca ttg 896

Ile Cys Val Glu Pro Thr Ser Gln Lys Leu Met Pro Gly Ser Thr Leu

230

235

240

gtt tta cag tgt gtt gct gtt gga agc cct att cct cac tac cag tgg 944

Val Leu Gln Cys Val Ala Val Gly Ser Pro Ile Pro His Tyr Gln Trp

245

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255

260

ttc aaa aat gaa tta cca tta aca cat gag acc aaa aag cta tac atg 992

Phe Lys Asn Glu Leu Pro Leu Thr His Glu Thr Lys Lys Leu Tyr Met

265

270

275

gtg cct tat gtg gat ttg gaa cac caa gga acc tac tgg tgt cat gta 1040

Val Pro Tyr Val Asp Leu Glu His Gln Gly Thr Tyr Trp Cys His Val
 280 285 290

tat aat gat cga gac agt caa gat agc aag aag gta gaa atc atc ata 1088
 Tyr Asn Asp Arg Asp Ser Gln Asp Ser Lys Lys Val Glu Ile Ile Ile
 295 300 305

gga aga aca gat gag gca gtg gag tgc act gaa gat gaa tta aat aat 1136
 Gly Arg Thr Asp Glu Ala Val Glu Cys Thr Glu Asp Glu Leu Asn Asn
 310 315 320

ctt ggt cat cct gat aat aaa gag caa aca act gac cag cct ttg gcg 1184
 Leu Gly His Pro Asp Asn Lys Glu Gln Thr Thr Asp Gln Pro Leu Ala
 325 330 335 340

aag gac aag gtt gcc ctt ttg ata gga aat atg aat tac cgg gag cac 1232
 Lys Asp Lys Val Ala Leu Leu Ile Gly Asn Met Asn Tyr Arg Glu His
 345 350 355

ccc aag ctc aaa gct cct ttg gtg gat gtg tac gaa ttg act aac tta 1280
 Pro Lys Leu Lys Ala Pro Leu Val Asp Val Tyr Glu Leu Thr Asn Leu
 360 365 370

ctg aga cag ctg gac ttc aaa gtg gtt tca ctg ttg gat ctt act gaa 1328
 Leu Arg Gln Leu Asp Phe Lys Val Val Ser Leu Leu Asp Leu Thr Glu
 375 380 385

tat gag atg cgt aat gct gtg gat gag ttt tta ctc ctt tta gac aag 1376
 Tyr Glu Met Arg Asn Ala Val Asp Glu Phe Leu Leu Leu Leu Asp Lys

390	395	400	
gga gta tat ggg tta tta tat tat gca gga cat ggt tat gaa aat ttt			1424
Gly Val Tyr Gly Leu Leu Tyr Tyr Ala Gly His Gly Tyr Glu Asn Phe			
405	410	415	420
ggg aac agc ttc atg gtc ccc gtt gat gct cca aat cca tat agg tct			1472
Gly Asn Ser Phe Met Val Pro Val Asp Ala Pro Asn Pro Tyr Arg Ser			
425	430	435	
gaa aat tgt ctg tgt gta caa aat ata ctg aaa ttg atg caa gaa aaa			1520
Glu Asn Cys Leu Cys Val Gln Asn Ile Leu Lys Leu Met Gln Glu Lys			
440	445	450	
gaa act gga ctt aat gtg ttc tta ttg gat atg tgt agg aaa aga aat			1568
Glu Thr Gly Leu Asn Val Phe Leu Leu Asp Met Cys Arg Lys Arg Asn			
455	460	465	
gac tac gat gat acc att cca atc ttg gat gca cta aaa gtc acc gcc			1616
Asp Tyr Asp Asp Thr Ile Pro Ile Leu Asp Ala Leu Lys Val Thr Ala			
470	475	480	
aat att gtg ttt gga tat gcc acg tgt caa gga gca gaa gct ttt gaa			1664
Asn Ile Val Phe Gly Tyr Ala Thr Cys Gln Gly Ala Glu Ala Phe Glu			
485	490	495	500
atc cag cat tct gga ttg gca aat gga atc ttt atg aaa ttt tta aaa			1712
Ile Gln His Ser Gly Leu Ala Asn Gly Ile Phe Met Lys Phe Leu Lys			
505	510	515	

gac aga tta tta gaa gat aag aaa atc act gtg tta ctg gat gaa gtt 1760

Asp Arg Leu Leu Glu Asp Lys Lys Ile Thr Val Leu Leu Asp Glu Val

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525

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gca gaa gat atg ggt aag tgt cac ctt acc aaa ggc aaa cag gct cta 1808

Ala Glu Asp Met Gly Lys Cys His Leu Thr Lys Gly Lys Gln Ala Leu

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gag att cga agt agt tta tct gag aag aga gca ctt act gat cca ata 1856

Glu Ile Arg Ser Ser Leu Ser Glu Lys Arg Ala Leu Thr Asp Pro Ile

550

555

560

cag gga aca gaa tat tct gct gaa tct ctt gtg cgg aat cta cag tgg 1904

Gln Gly Thr Glu Tyr Ser Ala Glu Ser Leu Val Arg Asn Leu Gln Trp

565

570

575

580

gcc aag gct cat gaa ctt cca gaa agt atg tgt ctt aag ttt gac tgt 1952

Ala Lys Ala His Glu Leu Pro Glu Ser Met Cys Leu Lys Phe Asp Cys

585

590

595

ggc gtt cag att caa tta gga ttt gca gct gag ttt tcc aat gtc atg 2000

Gly Val Gln Ile Gln Leu Gly Phe Ala Ala Glu Phe Ser Asn Val Met

600

605

610

atc atc tat aca agt ata gtt tac aaa cca ccg gag ata ata atg tgt 2048

Ile Ile Tyr Thr Ser Ile Val Tyr Lys Pro Pro Glu Ile Ile Met Cys

615

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625

gat gcc tac gtt act gat ttt cca ctt gat cta gat att gat cca aaa 2096
Asp Ala Tyr Val Thr Asp Phe Pro Leu Asp Leu Asp Ile Asp Pro Lys
630 635 640

gat gca aat aaa ggc aca cct gaa gaa act ggc agc tac ttg gta tca 2144
Asp Ala Asn Lys Gly Thr Pro Glu Glu Thr Gly Ser Tyr Leu Val Ser
645 650 655 660

aag gat ctt ccc aag cat tgc ctc tat acc aga ctc agt tca ctg caa 2192
Lys Asp Leu Pro Lys His Cys Leu Tyr Thr Arg Leu Ser Ser Leu Gln
665 670 675

aaa tta aag gaa cat cta gtc ttc aca gta tgt tta tca tat cag tac 2240
Lys Leu Lys Glu His Leu Val Phe Thr Val Cys Leu Ser Tyr Gln Tyr
680 685 690

tca gga ttg gaa gat act gta gag gac aag cag gaa gtg aat gtt ggg 2288
Ser Gly Leu Glu Asp Thr Val Glu Asp Lys Gln Glu Val Asn Val Gly
695 700 705

aaa cct ctc att gct aaa tta gac atg cat cga ggt ttg gga agg aag 2336
Lys Pro Leu Ile Ala Lys Leu Asp Met His Arg Gly Leu Gly Arg Lys
710 715 720

act tgc ttt caa act tgt ctt atg tct aat ggt cct tac cag agt tct 2384
Thr Cys Phe Gln Thr Cys Leu Met Ser Asn Gly Pro Tyr Gln Ser Ser
725 730 735 740

gca gcc acc tca gga gga gca ggg cat tat cac tca ttg caa gac cca 2432

Ala Ala Thr Ser Gly Gly Ala Gly His Tyr His Ser Leu Gln Asp Pro
 745 750 755

ttc cat ggt gtt tac cat tca cat cct ggt aat cca agt aat gtt aca 2480
 Phe His Gly Val Tyr His Ser His Pro Gly Asn Pro Ser Asn Val Thr
 760 765 770

cca gca gat agc tgt cat tgc agc cgg act cca gat gca ttt att tca 2528
 Pro Ala Asp Ser Cys His Cys Ser Arg Thr Pro Asp Ala Phe Ile Ser
 775 780 785

agt ttc gct cac cat gct tca tgt cat ttt agt aga agt aat gtg cca 2576
 Ser Phe Ala His His Ala Ser Cys His Phe Ser Arg Ser Asn Val Pro
 790 795 800

gta gag aca act gat gaa ata cca ttt agt ttc tct gac agg ctc aga 2624
 Val Glu Thr Thr Asp Glu Ile Pro Phe Ser Phe Ser Asp Arg Leu Arg
 805 810 815 820

att tct gaa aaa tgacctcctt gttttgaaa gttagcataa ttttagatgc 2676
 Ile Ser Glu Lys

ctgtgaaata gtaactgcact tacataaagt gagacattgt gaaaaggcaa atttgtatat 2736

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ttacattatt taattacaga cttcctcttt ct 2828

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<212> PRT

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<400> 133

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20 25 30

Glu Val Ala Ser Ile Leu Gln Ala Asp Leu Gln Asn Gly Leu Asn Lys

35 40 45

Cys Glu Val Ser His Arg Arg Ala Phe His Gly Trp Asn Glu Phe Asp

50 55 60

Ile Ser Glu Asp Glu Pro Leu Trp Lys Lys Tyr Ile Ser Gln Phe Lys

65 70 75 80

Asn Pro Leu Ile Met Leu Leu Leu Ala Ser Ala Val Ile Ser Val Leu

85 90 95

Met His Gln Phe Asp Asp Ala Val Ser Ile Thr Val Ala Ile Leu Ile

100 105 110

Val Val Thr Val Ala Phe Val Gln Glu Tyr Arg Ser Glu Lys Ser Leu

115 120 125

Glu Glu Leu Ser Lys Leu Val Pro Pro Glu Cys His Cys Val Arg Glu

130

135

140

Gly Lys Leu Glu His Thr Leu Ala Arg Asp Leu Val Pro Gly Asp Thr

145

150

155

160

Val Cys Leu Ser Val Gly Asp Arg Val Pro Ala Asp Leu Arg Leu Phe

165

170

175

Glu Ala Val Asp Leu Ser Ile Asp Glu Ser Ser Leu Thr Gly Glu Thr

180

185

190

Thr Pro Cys Ser Lys Val Thr Ala Pro Gln Pro Ala Ala Thr Asn Gly

195

200

205

Asp Leu Ala Ser Arg Ser Asn Ile Ala Phe Met Gly Thr Leu Val Arg

210

215

220

Cys Gly Lys Ala Lys Gly Val Val Ile Gly Thr Gly Glu Asn Ser Glu

225

230

235

240

Phe Gly Glu Val Phe Lys Met Met Gln Ala Glu Glu Ala Pro Lys Thr

245

250

255

Pro Leu Gln Lys Ser Met Asp Leu Leu Gly Lys Gln Leu Ser Phe Tyr

260

265

270

Ser Phe Gly Ile Ile Gly Ile Ile Met Leu Val Gly Trp Leu Leu Gly

275

280

285

Lys Asp Ile Leu Glu Met Phe Thr Ile Ser Val Ser Leu Ala Val Ala

290

295

300

Ala Ile Pro Glu Gly Leu Pro Ile Val Val Thr Val Thr Leu Ala Leu

305

310

315

320

Gly Val Met Arg Met Val Lys Lys Arg Ala Ile Val Lys Lys Leu Pro

325

330

335

Ile Val Glu Thr Leu Gly Cys Cys Asn Val Ile Cys Ser Asp Lys Thr

340

345

350

Gly Thr Leu Thr Lys Asn Glu Met Thr Val Thr His Ile Phe Thr Ser

355

360

365

Asp Gly Leu His Ala Glu Val Thr Gly Val Gly Tyr Asn Gln Phe Gly

370

375

380

Glu Val Ile Val Asp Gly Asp Val Val His Gly Phe Tyr Asn Pro Ala

385

390

395

400

Val Ser Arg Ile Val Glu Ala Gly Cys Val Cys Asn Asp Ala Val Ile

405

410

415

Arg Asn Asn Thr Leu Met Gly Lys Pro Thr Glu Gly Ala Leu Ile Ala

420

425

430

Leu Ala Met Lys Met Gly Leu Asp Gly Leu Gln Gln Asp Tyr Ile Arg
435 440 445

Lys Ala Glu Tyr Pro Phe Ser Ser Glu Gln Lys Trp Met Ala Val Lys
450 455 460

Cys Val His Arg Thr Gln Gln Asp Arg Pro Glu Ile Cys Phe Met Lys
465 470 475 480

Gly Ala Tyr Glu Gln Val Ile Lys Tyr Cys Thr Thr Tyr Gln Ser Lys
485 490 495

Gly Gln Thr Leu Thr Leu Thr Gln Gln Gln Arg Asp Val Tyr Gln Gln
500 505 510

Glu Lys Ala Arg Met Gly Ser Ala Gly Leu Arg Val Leu Ala Leu Ala
515 520 525

Ser Gly Pro Glu Leu Gly Gln Leu Thr Phe Leu Gly Leu Val Gly Ile
530 535 540

Ile Asp Pro Pro Arg Thr Gly Val Lys Glu Ala Val Thr Thr Leu Ile
545 550 555 560

Ala Ser Gly Val Ser Ile Lys Met Ile Thr Gly Asp Ser Gln Glu Thr
565 570 575

Ala Val Ala Ile Ala Ser Arg Leu Gly Leu Tyr Ser Lys Thr Ser Gln
580 585 590

Ser Val Ser Gly Glu Glu Ile Asp Ala Met Asp Val Gln Gln Leu Ser
595 600 605

Gln Ile Val Pro Lys Val Ala Val Phe Tyr Arg Ala Ser Pro Arg His
610 615 620

Lys Met Lys Ile Ile Lys Ser Leu Gln Lys Asn Gly Ser Val Val Ala
625 630 635 640

Met Thr Gly Asp Gly Val Asn Asp Ala Val Ala Leu Lys Ala Ala Asp
645 650 655

Ile Gly Val Ala Met Gly Gln Thr Gly Thr Asp Val Cys Lys Glu Ala
660 665 670

Ala Asp Met Ile Leu Val Asp Asp Asp Phe Gln Thr Ile Met Ser Ala
675 680 685

Ile Glu Glu Gly Lys Gly Ile Tyr Asn Asn Ile Lys Asn Phe Val Arg
690 695 700

Phe Gln Leu Ser Thr Ser Ile Ala Ala Leu Thr Leu Ile Ser Leu Ala
705 710 715 720

Thr Leu Met Asn Phe Pro Asn Pro Leu Asn Ala Met Gln Ile Leu Trp
725 730 735

Ile Asn Ile Ile Met Asp Gly Pro Pro Ala Gln Ser Leu Gly Val Glu

740

745

750

Pro Val Asp Lys Asp Val Ile Arg Lys Pro Pro Arg Asn Trp Lys Asp

755

760

765

Ser Ile Leu Thr Lys Asn Leu Ile Leu Lys Ile Leu Val Ser Ser Ile

770

775

780

Ile Ile Val Cys Gly Thr Leu Phe Val Phe Trp Arg Glu Leu Arg Asp

785

790

795

800

Asn Val Ile Thr Pro Arg Asp Thr Thr Met Thr Phe Thr Cys Phe Val

805

810

815

Phe Phe Asp Met Phe Asn Ala Leu Ser Ser Arg Ser Gln Thr Lys Ser

820

825

830

Val Phe Glu Ile Gly Leu Cys Ser Asn Arg Met Phe Cys Tyr Ala Val

835

840

845

Leu Gly Ser Ile Met Gly Gln Leu Leu Val Ile Tyr Phe Pro Pro Leu

850

855

860

Gln Lys Val Phe Gln Thr Glu Ser Leu Ser Ile Leu Asp Leu Leu Phe

865

870

875

880

Leu Leu Gly Leu Thr Ser Ser Val Cys Ile Val Ala Glu Ile Ile Lys

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890

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Lys Val Glu Arg Ser Arg Glu Lys Ile Gln Lys His Val Ser Ser Thr

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Ser Ser Ser Phe Leu Glu Val

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gagcaggctc ccgctcgcga ccgtgcccc gcgagcagct cctcttctcc cgaggcgcgc 180

ggggcgcccc cgcgagcccc ggggtgaga cccgcagcc tggaggaggg ctgtccgggg 240

ctttggatgc tgctgctagg ggtggtgga gcagccgtgg gacgcgtggc cgggagcggg 300

ggtgacagcc tgggattccg ggggttctc ttcttgctcc tctctctc cctctattc 360

ccagtgtggc cgtggctgac actaaagact ttgtagccat caacccgagt gcagtttcga 420

tggaaa atg aag gtt gca cgt ttt caa aaa ata cct aat ggt gaa aat 468

Met Lys Val Ala Arg Phe Gln Lys Ile Pro Asn Gly Glu Asn

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gag aca atg att cct gta ttg aca tca aaa aaa gca agt gaa tta cca 516

Glu Thr Met Ile Pro Val Leu Thr Ser Lys Lys Ala Ser Glu Leu Pro

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25

- 30

gtc agt gaa gtt gca agc att ctc caa gct gat ctt cag aat ggt cta 564

Val Ser Glu Val Ala Ser Ile Leu Gln Ala Asp Leu Gln Asn Gly Leu

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aac aaa tgt gaa gtt agt cat agg cga gcc ttt cat ggc tgg aat gag 612

Asn Lys Cys Glu Val Ser His Arg Arg Ala Phe His Gly Trp Asn Glu

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ttt gat att agt gaa gat gag cca ctg tgg aag aag tat att tct cag 660

Phe Asp Ile Ser Glu Asp Glu Pro Leu Trp Lys Lys Tyr Ile Ser Gln

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70

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ttt aaa aat ccc ctt att atg ctg ctt ctg gct tct gca gtc atc agt 708

Phe Lys Asn Pro Leu Ile Met Leu Leu Leu Ala Ser Ala Val Ile Ser

80

85

90

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Val Leu Met His Gln Phe Asp Asp Ala Val Ser Ile Thr Val Ala Ile

95

100

105

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ctt atc gtt gtt aca gtt gcc ttt gtt cag gaa tat cgt tca gaa aaa 804

Leu Ile Val Val Thr Val Ala Phe Val Gln Glu Tyr Arg Ser Glu Lys

115

120

125

tct ctt gaa gaa ttg agt aaa ctt gtg cca cca gaa tgc cat tgt gtg 852

Ser Leu Glu Glu Leu Ser Lys Leu Val Pro Pro Glu Cys His Cys Val

130

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cgt gaa gga aaa ttg gag cat aca ctt gcc cga gac ttg gtt cca ggt 900

Arg Glu Gly Lys Leu Glu His Thr Leu Ala Arg Asp Leu Val Pro Gly

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gat aca gtt tgc ctt tct gtt ggg gat aga gtt cct gct gac tta cgc 948

Asp Thr Val Cys Leu Ser Val Gly Asp Arg Val Pro Ala Asp Leu Arg

160

165

170

ttg ttt gag gct gtg gat ctt tcc att gat gag tcc agc ttg aca ggt 996

Leu Phe Glu Ala Val Asp Leu Ser Ile Asp Glu Ser Ser Leu Thr Gly

175

180

185

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gag aca acg cct tgt tct aag gtg aca gct cct cag cca gct gca act 1044

Glu Thr Thr Pro Cys Ser Lys Val Thr Ala Pro Gln Pro Ala Ala Thr

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aat gga gat ctt gca tcg aga agt aac att gcc ttt atg gga aca ctg 1092

Asn Gly Asp Leu Ala Ser Arg Ser Asn Ile Ala Phe Met Gly Thr Leu

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215

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gtc aga tgt ggc aaa gca aag ggt gtt gtc att gga aca gga gaa aat 1140
Val Arg Cys Gly Lys Ala Lys Gly Val Val Ile Gly Thr Gly Glu Asn

225

230

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tct gaa ttt ggg gag gtt ttt aaa atg atg caa gca gaa gag gca cca 1188
Ser Glu Phe Gly Glu Val Phe Lys Met Met Gln Ala Glu Glu Ala Pro

240

245

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aaa acc cct ctg cag aag agc atg gac ctc tta gga aaa caa ctt tcc 1236
Lys Thr Pro Leu Gln Lys Ser Met Asp Leu Leu Gly Lys Gln Leu Ser

255

260

265

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ttt tac tcc ttt ggt ata ata gga atc atc atg ttg gtt ggc tgg tta 1284
Phe Tyr Ser Phe Gly Ile Ile Gly Ile Ile Met Leu Val Gly Trp Leu

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ctg gga aaa gat atc ctg gaa atg ttt act att agt gta agt ttg gct 1332
Leu Gly Lys Asp Ile Leu Glu Met Phe Thr Ile Ser Val Ser Leu Ala

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gta gca gca att cct gaa ggt ctc ccc att gtg gtc aca gtg acg cta 1380
Val Ala Ala Ile Pro Glu Gly Leu Pro Ile Val Val Thr Val Thr Leu

305

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315

gct ctt ggt gtt atg aga atg gtg aag aaa agg gcc att gtg aaa aag 1428
Ala Leu Gly Val Met Arg Met Val Lys Lys Arg Ala Ile Val Lys Lys

320

325

330

ctg cct att gtt gaa act ctg ggc tgc tgt aat gtg att tgt tca gat 1476

Leu Pro Ile Val Glu Thr Leu Gly Cys Cys Asn Val Ile Cys Ser Asp
 335 340 345 350

aaa act gga aca ctg acg aag aat gaa atg act gtt act cac ata ttt 1524
 Lys Thr Gly Thr Leu Thr Lys Asn Glu Met Thr Val Thr His Ile Phe
 355 360 365

act tca gat ggt ctg cat gct gag gtt act gga gtt ggc tat aat caa 1572
 Thr Ser Asp Gly Leu His Ala Glu Val Thr Gly Val Gly Tyr Asn Gln
 370 375 380

ttt ggg gaa gtg att gtt gat ggt gat gtt gtt cat gga ttc tat aac 1620
 Phe Gly Glu Val Ile Val Asp Gly Asp Val Val His Gly Phe Tyr Asn
 385 390 395

cca gct gtt agc aga att gtt gag gcg ggc tgt gtg tgc aat gat gct 1668
 Pro Ala Val Ser Arg Ile Val Glu Ala Gly Cys Val Cys Asn Asp Ala
 400 405 410

gta att aga aac aat act cta atg ggg aag cca aca gaa ggg gcc tta 1716
 Val Ile Arg Asn Asn Thr Leu Met Gly Lys Pro Thr Glu Gly Ala Leu
 415 420 425 430

att gct ctt gca atg aag atg ggt ctt gat gga ctt caa caa gac tac 1764
 Ile Ala Leu Ala Met Lys Met Gly Leu Asp Gly Leu Gln Gln Asp Tyr
 435 440 445

atc aga aaa gct gaa tac cct ttt agc tct gag caa aag tgg atg gct 1812
 Ile Arg Lys Ala Glu Tyr Pro Phe Ser Ser Glu Gln Lys Trp Met Ala

450

455

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gtt aag tgt gta cac cga aca cag cag gac aga cca gag att tgt ttt 1860

Val Lys Cys Val His Arg Thr Gln Gln Asp Arg Pro Glu Ile Cys Phe

465

470

475

atg aaa ggt gct tac gaa caa gta att aag tac tgt act aca tac cag 1908

Met Lys Gly Ala Tyr Glu Gln Val Ile Lys Tyr Cys Thr Thr Tyr Gln

480

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490

agc aaa ggg cag acc ttg aca ctt act cag cag cag aga gat gtg tac 1956

Ser Lys Gly Gln Thr Leu Thr Leu Thr Gln Gln Gln Arg Asp Val Tyr

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caa caa gag aag gca cgc atg ggc tca gcg gga ctc aga gtt ctt gct 2004

Gln Gln Glu Lys Ala Arg Met Gly Ser Ala Gly Leu Arg Val Leu Ala

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ttg gct tct ggt cct gaa ctg gga cag ctg aca ttt ctt ggc ttg gtg 2052

Leu Ala Ser Gly Pro Glu Leu Gly Gln Leu Thr Phe Leu Gly Leu Val

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gga atc att gat cca cct aga act ggt gtg aaa gaa gct gtt aca aca 2100

Gly Ile Ile Asp Pro Pro Arg Thr Gly Val Lys Glu Ala Val Thr Thr

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ctc att gcc tca gga gta tca ata aaa atg att act gga gat tca cag 2148

Leu Ile Ala Ser Gly Val Ser Ile Lys Met Ile Thr Gly Asp Ser Gln

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gag act gca gtt gca atc gcc agt cgt ctg gga ttg tat tcc aaa act 2196

Glu Thr Ala Val Ala Ile Ala Ser Arg Leu Gly Leu Tyr Ser Lys Thr

575 580 585 590

tcc cag tca gtc tca gga gaa gaa ata gat gca atg gat gtt cag cag 2244

Ser Gln Ser Val Ser Gly Glu Glu Ile Asp Ala Met Asp Val Gln Gln

595 600 605

ctt tca caa ata gta cca aag gtt gca gta ttt tac aga gct agc cca 2292

Leu Ser Gln Ile Val Pro Lys Val Ala Val Phe Tyr Arg Ala Ser Pro

610 615 620

agg cac aag atg aaa att att aag tcg cta cag aag aac ggt tca gtt 2340

Arg His Lys Met Lys Ile Ile Lys Ser Leu Gln Lys Asn Gly Ser Val

625 630 635

gta gcc atg aca gga gat gga gta aat gat gca gtt gct ctg aag gct 2388

Val Ala Met Thr Gly Asp Gly Val Asn Asp Ala Val Ala Leu Lys Ala

640 645 650

gca gac att gga gtt gcg atg ggc cag act ggt aca gat gtt tgc aaa 2436

Ala Asp Ile Gly Val Ala Met Gly Gln Thr Gly Thr Asp Val Cys Lys

655 660 665 670

gag gca gca gac atg atc cta gtg gat gat gat ttt caa acc ata atg 2484

Glu Ala Ala Asp Met Ile Leu Val Asp Asp Asp Phe Gln Thr Ile Met

675 680 685

tct gca atc gaa gag ggt aaa ggg att tat aat aac att aaa aat ttc 2532
Ser Ala Ile Glu Glu Gly Lys Gly Ile Tyr Asn Asn Ile Lys Asn Phe

690

695

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gtt aga ttc cag ctg agc acg agt ata gca gca tta act tta atc tca 2580
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705

710

715

ttg gct aca tta atg aac ttt cct aat cct ctc aat gcc atg cag att 2628
Leu Ala Thr Leu Met Asn Phe Pro Asn Pro Leu Asn Ala Met Gln Ile

720

725

730

ttg tgg atc aat att att atg gat gga ccc cca gct cag agc ctt gga 2676
Leu Trp Ile Asn Ile Ile Met Asp Gly Pro Pro Ala Gln Ser Leu Gly

735

740

745

750

gta gaa cca gtg gat aaa gat gtc att cgt aaa cct cct cgc aac tgg 2724
Val Glu Pro Val Asp Lys Asp Val Ile Arg Lys Pro Pro Arg Asn Trp

755

760

765

aaa gac agc att ttg act aaa aac ttg ata ctt aaa ata ctt gtt tca 2772
Lys Asp Ser Ile Leu Thr Lys Asn Leu Ile Leu Lys Ile Leu Val Ser

770

775

780

tca ata atc att gtt tgt ggg act ttg ttt gtc ttc tgg cgt gag cta 2820
Ser Ile Ile Ile Val Cys Gly Thr Leu Phe Val Phe Trp Arg Glu Leu

785

790

795

cga gac aat gtg att aca cct cga gac aca aca atg acc ttc aca tgc 2868

Arg Asp Asn Val Ile Thr Pro Arg Asp Thr Thr Met Thr Phe Thr Cys

800

805

810

ttt gtg ttt ttt gac atg ttc aat gca cta agt tcc aga tcc cag acc 2916

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820

825

830

aag tct gtg ttt gag att gga ctc tgc agt aat aga atg ttt tgc tat 2964

Lys Ser Val Phe Glu Ile Gly Leu Cys Ser Asn Arg Met Phe Cys Tyr

835

840

845

gca gtt ctt gga tcc atc atg gga caa tta cta gtt att tac ttt cct 3012

Ala Val Leu Gly Ser Ile Met Gly Gln Leu Leu Val Ile Tyr Phe Pro

850

855

860

ccg ctt cag aag gtt ttt cag act gag agc cta agc ata ctg gat ctg 3060

Pro Leu Gln Lys Val Phe Gln Thr Glu Ser Leu Ser Ile Leu Asp Leu

865

870

875

ttg ttt ctt ttg ggt ctc acc tca tca gtg tgc ata gtg gca gaa att 3108

Leu Phe Leu Leu Gly Leu Thr Ser Ser Val Cys Ile Val Ala Glu Ile

880

885

890

ata aag aag gtt gaa agg agc agg gaa aag atc cag aag cat gtt agt 3156

Ile Lys Lys Val Glu Arg Ser Arg Glu Lys Ile Gln Lys His Val Ser

895

900

905

910

tgc aca tca tca tct ttt ctt gaa gta tgatgcatat tgcattattt 3203

Ser Thr Ser Ser Ser Phe Leu Glu Val

915

tatttgcaaa ctaggaattg cagtctgagg atcattttaga agggcaagtt caagaggata 3263

tgaagatttg agaacttttt aactattcat tgactaaaaa tgaacattaa tgttaaagac 3323

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aattaaaaag gcaaaacctg aaccaccttc tgcacttaa gaagtctaac agtacaata 3503

cactatctat cttagalaga tatatttttt ttatttttta aatattgtac tatttatggt 3563

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<212> PRT

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<400> 135

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Arg Val Glu Met Glu Asp Ala His Thr Ala Val Ile Gly Leu Pro Ser

35

40

45

Gly Leu Glu Ser Trp Ser Phe Phe Ala Val Tyr Asp Gly His Ala Gly

50

55

60

Ser Gln Val Ala Lys Tyr Cys Cys Glu His Leu Leu Asp His Ile Thr

65

70

75

80

Asn Asn Gln Asp Phe Lys Gly Ser Ala Gly Ala Pro Ser Val Glu Asn

85

90

95

Val Lys Asn Gly Ile Arg Thr Gly Phe Leu Glu Ile Asp Glu His Met

100

105

110

Arg Val Met Ser Glu Lys Lys His Gly Ala Asp Arg Ser Gly Ser Thr

115

120

125

Ala Val Gly Val Leu Ile Ser Pro Gln His Thr Tyr Phe Ile Asn Cys

130

135

140

Gly Asp Ser Arg Gly Leu Leu Cys Arg Asn Arg Lys Val His Phe Phe

145

150

155

160

Thr Gln Asp His Lys Pro Ser Asn Pro Leu Glu Lys Glu Arg Ile Gln

165

170

175

Asn Ala Gly Gly Ser Val Met Ile Gln Arg Val Asn Gly Ser Leu Ala

180

185

190

Val Ser Arg Ala Leu Gly Asp Phe Asp Tyr Lys Cys Val His Gly Lys

195

200

205

Gly Pro Thr Glu Gln Leu Val Ser Pro Glu Pro Glu Val His Asp Ile

210

215

220

Glu Arg Ser Glu Glu Asp Asp Gln Phe Ile Ile Leu Ala Cys Asp Gly

225

230

235

- 240

Ile Trp Asp Val Met Gly Asn Glu Glu Leu Cys Asp Phe Val Arg Ser

245

250

255

Arg Leu Glu Val Thr Asp Asp Leu Glu Lys Val Cys Asn Glu Val Val

260

265

270

Asp Thr Cys Leu Tyr Lys Gly Ser Arg Asp Asn Met Ser Val Ile Leu

275

280

285

Ile Cys Phe Pro Asn Ala Pro Lys Val Ser Pro Glu Ala Val Lys Lys

290

295

300

Glu Ala Glu Leu Asp Lys Tyr Leu Glu Cys Arg Val Glu Glu Ile Ile

305

310

315

320

Lys Lys Gln Gly Glu Gly Val Pro Asp Leu Val His Val Met Arg Thr

325

330

335

Leu Ala Ser Glu Asn Ile Pro Ser Leu Pro Pro Gly Gly Glu Leu Ala

340

345

350

Ser Lys Arg Asn Val Ile Glu Ala Val Tyr Asn Arg Leu Asn Pro Tyr

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Lys Asn Asp Asp Thr Asp Ser Thr Ser Thr Asp Asp Met Trp

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375

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<210> 136

<211> 2467

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (444).. (1589)

<400> 136

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tctagacagc tgaggcgcga aagcgatgag tctcggctc ttctctctcc ttctccggga 180

cccgtctct gctccctct ccaacgccc gatgactga gccgcgagg cgccgacagc 240

cgggggcccc gacgcagccc ggctctctcc ctctccgcc ccttccccag cctgacctgg 300

cccgccgcig cagcgggtgac cctcccccg gctgccgccg tcgccgccgc ggigaccccc 360

tccccggctg ccgccgccgc cgcctcggcc gaccaggac ctgccgcct gcggctgctc 420

cggacctaga ggatcaagac ata atg gga gca ttt tta gac aag cca aag atg 473

Met Gly Ala Phe Leu Asp Lys Pro Lys Met

1

5

10

gaa aag cat aat gcc cag ggg cag ggt aat ggg ttg cga tat ggg cta 521

Glu Lys His Asn Ala Gln Gly Gln Gly Asn Gly Leu Arg Tyr Gly Leu

15

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25

agc agc atg caa ggc tgg cgt gtt gaa atg gag gat gca cat acg gct 569

Ser Ser Met Gln Gly Trp Arg Val Glu Met Glu Asp Ala His Thr Ala

30

35

40

gtg atc ggt ttg cca agt gga ctt gaa tcg tgg tca ttc ttt gct gtg 617

Val Ile Gly Leu Pro Ser Gly Leu Glu Ser Trp Ser Phe Phe Ala Val

45

50

55

tat gat ggg cat gct ggt tct cag gtt gcc aaa tac tgc tgt gag cat 665

Tyr Asp Gly His Ala Gly Ser Gln Val Ala Lys Tyr Cys Cys Glu His

60

65

70

ttg tta gat cac atc acc aat aac cag gat ttt aaa ggg tct gca gga 713

Leu Leu Asp His Ile Thr Asn Asn Gln Asp Phe Lys Gly Ser Ala Gly

75

80

85

90

gca cct tct gtg gaa aat gta aag aat gga atc aga aca ggt ttt ctg 761

Ala Pro Ser Val Glu Asn Val Lys Asn Gly Ile Arg Thr Gly Phe Leu

95

100

105

gag att gat gaa cac atg aga gtt atg tca gag aag aaa cat ggt gca 809

Glu Ile Asp Glu His Met Arg Val Met Ser Glu Lys Lys His Gly Ala

110

115

120

gat aga agt ggg tca aca gct gta ggt gtc tta att tct ccc caa cat 857

Asp Arg Ser Gly Ser Thr Ala Val Gly Val Leu Ile Ser Pro Gln His

125

130

135

act tat ttc att aac tgt gga gac tca aga ggt tta ctt tgt agg aac 905

Thr Tyr Phe Ile Asn Cys Gly Asp Ser Arg Gly Leu Leu Cys Arg Asn

140

145

150

agg aaa gtt cat ttc ttc aca caa gat cac aaa cca agt aat ccg ctg 953

Arg Lys Val His Phe Phe Thr Gln Asp His Lys Pro Ser Asn Pro Leu

155

160

165

170

gag aaa gaa cga att cag aat gca ggt ggc tct gta atg att cag cgt 1001

Glu Lys Glu Arg Ile Gln Asn Ala Gly Gly Ser Val Met Ile Gln Arg

175

180

185

gtg aat ggc tct ctg gct gta tcg agg gcc ctt ggg gat ttt gat tac 1049

Val Asn Gly Ser Leu Ala Val Ser Arg Ala Leu Gly Asp Phe Asp Tyr

190

195

200

aaa tgt gtc cat gga aaa ggt cct act gag cag ctt gtc tca cca gag 1097

Lys Cys Val His Gly Lys Gly Pro Thr Glu Gln Leu Val Ser Pro Glu

205	210	215	
cct gaa gtc cat gat att gaa aga tct gaa gaa gat gat cag ttc att			1145
Pro Glu Val His Asp Ile Glu Arg Ser Glu Glu Asp Asp Gln Phe Ile			
220	225	230	
atc ctt gca tgt gat ggt atc tgg gat gtt atg gga aat gaa gag ctc			1193
Ile Leu Ala Cys Asp Gly Ile Trp Asp Val Met Gly Asn Glu Glu Leu			
235	240	245	250
tgt gat ttt gta aga tcc aga ctt gaa gtc act gat gac ctt gag aaa			1241
Cys Asp Phe Val Arg Ser Arg Leu Glu Val Thr Asp Asp Leu Glu Lys			
255	260	265	
gtt tgc aat gaa gta gtc gac acc tgt ttg tat aag gga agt cga gac			1289
Val Cys Asn Glu Val Val Asp Thr Cys Leu Tyr Lys Gly Ser Arg Asp			
270	275	280	
aac atg agt gtc att ttg atc tgt ttt cca aat gca ccc aaa gta tcg			1337
Asn Met Ser Val Ile Leu Ile Cys Phe Pro Asn Ala Pro Lys Val Ser			
285	290	295	
cca gaa gca gtg aag aag gag gca gag ttg gac aag tac ctg gaa tgc			1385
Pro Glu Ala Val Lys Lys Glu Ala Glu Leu Asp Lys Tyr Leu Glu Cys			
300	305	310	
aga gta gaa gaa atc ata aag aag cag ggg gaa ggc gtc ccc gac tta			1433
Arg Val Glu Glu Ile Ile Lys Lys Gln Gly Glu Gly Val Pro Asp Leu			
315	320	325	330

gtc cat gtg atg cgc aca tta gcg agt gag aac atc ccc agc ctc cca 1481

Val His Val Met Arg Thr Leu Ala Ser Glu Asn Ile Pro Ser Leu Pro

335

340

345

cca ggg ggt gaa ttg gca agc aag agg aat gtt att gaa gcc gtt tac 1529

Pro Gly Gly Glu Leu Ala Ser Lys Arg Asn Val Ile Glu Ala Val Tyr

350

355

360

aat aga ctg aat cct tac aaa aat gac gac act gac tct aca tca aca 1577

Asn Arg Leu Asn Pro Tyr Lys Asn Asp Asp Thr Asp Ser Thr Ser Thr

365

370

375

gat gat atg tgg taaaactgct catctagcca tggagtttac cttcacctcc 1629

Asp Asp Met Trp

380

aaaggagagt acagctcaac tttgttgaaa cttttaacat ccaccccaa ctttaaggaa 1689

ggggatatga catgggtgag aatgattaca tcagagaact tcagcagtac aacagctagc 1749

ccagaactga tttttttttt ttttttgtaa atttgagact tatgtaagcg tgatttcaaa 1809

ccataattcg tgttgtaa at cagactccag caatttttgt tgtatgattt tgttttttig 1869

taaagtgtaa ttgtccttgt acaaaatgct catattta at tatgaactgc tttaaatcac 1929

tatcaaagtt acaagaaatg ttggccttat tgtgtgatgc aacagatata tagccctttc 1989

aagtcagtgt gtgtttggac ttggggttgg aacagggaga gcagcagcca tgtcagctac 2049

acgctcaaat gtgcagatga ttatggaaaa taacctcaaa atcttcaaaa gcigaacatc 2109

caaggagtta ttgaaaacta tcttaaatgt tcttggtagg ggagttggca ttgttgataa 2169

agccagtcctt ttcatttaac tgtctttcag gatgttcctt cgttggttcc atgagtattg 2229

caggtaataa tacagtgtat tcataagaat ctcaatcttg gggctaaatg ccttgtttct 2289

ttgcacctct ttcaagtcct ttacatttaa ttactaatg ataagcagca gcttcctaca 2349

tatagtagga aactgccaca tttttgctat catgattggc tgggcctgct gctgttccta 2409

gtaagatatt ctgaattcca ttttatcaat aaagcttgat ttaacaaaca agaaactt 2467

<210> 137

<211> 358

<212> PRT

<213> Homo sapiens

<400> 137

Met Met Gln Arg Val Phe Arg Gly Lys Leu Leu Ser Asn Asp Glu Val

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10

15

Thr Ile Lys Tyr Lys Asp Glu Asp Gly Asp Leu Ile Thr Ile Phe Asp

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25

30

Ser Ser Asp Leu Ser Phe Ala Ile Gln Cys Ser Arg Ile Leu Lys Leu

35

40

45

Thr Leu Phe Val Asn Gly Gln Pro Arg Pro Leu Glu Ser Ser Gln Val

50

55

60

Lys Tyr Leu Arg Arg Glu Leu Ile Glu Leu Arg Asn Lys Val Asn Arg

65

70

75

80

Leu Leu Asp Ser Leu Glu Pro Pro Gly Glu Pro Gly Pro Ser Thr Asn

85

90

95

Ile Pro Glu Asn Asp Thr Val Asp Gly Arg Glu Glu Lys Ser Ala Ser

100

105

110

Asp Ser Ser Gly Lys Gln Ser Thr Gln Val Met Ala Ala Ser Met Ser

115

120

125

Ala Phe Asp Pro Leu Lys Asn Gln Asp Glu Ile Asn Lys Asn Val Met

130

135

140

Ser Ala Phe Gly Leu Thr Asp Asp Gln Val Ser Gly Pro Pro Ser Ala

145

150

155

160

Pro Ala Glu Asp Arg Ser Gly Thr Pro Asp Ser Ile Ala Ser Ser Ser

165

170

175

Ser Ala Ala His Pro Pro Gly Val Gln Pro Gln Gln Pro Pro Tyr Thr

180

185

190

Gly Ala Gln Thr Gln Ala Gly Gln Met Tyr Gln Gln Tyr Gln Gln Gln
195 200 205

Ala Gly Tyr Gly Ala Gln Gln Pro Gln Ala Pro Pro Gln Gln Pro Gln
210 215 220

Gln Tyr Gly Ile Gln Tyr Ser Ala Ser Tyr Ser Gln Gln Thr Gly Pro
225 230 235 240

Gln Gln Pro Gln Gln Phe Gln Gly Tyr Gly Gln Gln Pro Thr Ser Gln
245 250 255

Ala Pro Ala Pro Ala Phe Ser Gly Gln Pro Gln Gln Leu Pro Ala Gln
260 265 270

Pro Pro Gln Gln Tyr Gln Ala Ser Asn Tyr Pro Ala Gln Thr Tyr Thr
275 280 285

Ala Gln Thr Ser Gln Pro Thr Asn Tyr Thr Val Ala Pro Ala Ser Gln
290 295 300

Pro Gly Met Ala Pro Ser Gln Pro Gly Ala Tyr Gln Pro Arg Pro Gly
305 310 315 320

Phe Thr Ser Leu Pro Gly Ser Thr Met Thr Pro Pro Pro Ser Gly Pro
325 330 335

Asn Pro Tyr Ala Arg Asn Arg Pro Pro Phe Gly Gln Gly Tyr Thr Gln

340

345

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Pro Gly Pro Gly Tyr Arg

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<210> 138

<211> 1519

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (11).. (1084)

<400> 138

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Met Met Gln Arg Val Phe Arg Gly Lys Leu Leu Ser Asn

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gat gaa gta aca ata aag tat aaa gat gaa gat gga gat ctt ata aca 97

Asp Glu Val Thr Ile Lys Tyr Lys Asp Glu Asp Gly Asp Leu Ile Thr

15

20

25

att ttt gat agt tct gac ctt tcc ttt gca att cag tgc agt agg ata 145

Ile Phe Asp Ser Ser Asp Leu Ser Phe Ala Ile Gln Cys Ser Arg Ile

30

35

40

45

ctg aaa ctg aca tta ttt gtt aat ggc cag cca aga ccc ctt gaa tca 193

Leu Lys Leu Thr Leu Phe Val Asn Gly Gln Pro Arg Pro Leu Glu Ser
 50 55 60

agt cag gtg aaa tat ctc cgt cga gaa ctg ata gaa ctt cga aat aaa 241
 Ser Gln Val Lys Tyr Leu Arg Arg Glu Leu Ile Glu Leu Arg Asn Lys
 65 70 75

gtg aat cgt tta ttg gat agc ttg gaa cca cct gga gaa cca gga cct 289
 Val Asn Arg Leu Leu Asp Ser Leu Glu Pro Pro Gly Glu Pro Gly Pro
 80 85 90

tcc acc aat att cct gaa aat gat act gtg gat ggt agg gaa gaa aag 337
 Ser Thr Asn Ile Pro Glu Asn Asp Thr Val Asp Gly Arg Glu Glu Lys
 95 100 105

tct gct tct gat tct tct gga aaa cag tct act cag gtt atg gca gca 385
 Ser Ala Ser Asp Ser Ser Gly Lys Gln Ser Thr Gln Val Met Ala Ala
 110 115 120 125

agt atg tct gct ttt gat cct tta aaa aac caa gat gaa atc aat aaa 433
 Ser Met Ser Ala Phe Asp Pro Leu Lys Asn Gln Asp Glu Ile Asn Lys
 130 135 140

aat gtt atg tca gcg ttt ggc tta aca gat gat cag gtt tca ggg cca 481
 Asn Val Met Ser Ala Phe Gly Leu Thr Asp Asp Gln Val Ser Gly Pro
 145 150 155

ccc agt gct cct gca gaa gat cgt tca gga aca ccc gac agc att gct 529
 Pro Ser Ala Pro Ala Glu Asp Arg Ser Gly Thr Pro Asp Ser Ile Ala

160	165	170	
tcc tcc tcc tca gca gct cac cca cca ggc gtt cag cca cag cag cca	577		
Ser Ser Ser Ser Ala Ala His Pro Pro Gly Val Gln Pro Gln Gln Pro			
175	180	185	
cca tat aca gga gct cag act caa gca ggt cag atg tac caa cag tac	625		
Pro Tyr Thr Gly Ala Gln Thr Gln Ala Gly Gln Met Tyr Gln Gln Tyr			
190	195	200	205
cag caa cag gcc ggc tat ggt gca cag cag ccg cag gct cca cct cag	673		
Gln Gln Gln Ala Gly Tyr Gly Ala Gln Gln Pro Gln Ala Pro Pro Gln			
210	215	220	
cag cct caa cag tat ggt att cag tat tca gca agc tat agt cag cag	721		
Gln Pro Gln Gln Tyr Gly Ile Gln Tyr Ser Ala Ser Tyr Ser Gln Gln			
225	230	235	
act gga ccc caa caa cct cag cag ttc cag gga tat ggc cag caa cca	769		
Thr Gly Pro Gln Gln Pro Gln Gln Phe Gln Gly Tyr Gly Gln Gln Pro			
240	245	250	
act tcc cag gca cca gct cct gcc ttt tct ggt cag cct caa caa ctg	817		
Thr Ser Gln Ala Pro Ala Pro Ala Phe Ser Gly Gln Pro Gln Gln Leu			
255	260	265	
cct gct cag ccg cca cag cag tac cag gcg agc aat tat cct gca caa	865		
Pro Ala Gln Pro Pro Gln Gln Tyr Gln Ala Ser Asn Tyr Pro Ala Gln			
270	275	280	285

act tac act gcc caa act tct cag cct act aat tat act gtg gct cct 913

Thr Tyr Thr Ala Gln Thr Ser Gln Pro Thr Asn Tyr Thr Val Ala Pro

290

295

300

gcc tct caa cct gga atg gct cca agc caa cct ggg gcc tat caa cca 961

Ala Ser Gln Pro Gly Met Ala Pro Ser Gln Pro Gly Ala Tyr Gln Pro

305

310

315

aga cca ggt ttt act tca ctt cct gga agt acc atg acc cct cct cca 1009

Arg Pro Gly Phe Thr Ser Leu Pro Gly Ser Thr Met Thr Pro Pro Pro

320

325

330

agt ggg cct aat cct tat gcg cgt aac cgt cct ccc ttt ggt cag ggc 1057

Ser Gly Pro Asn Pro Tyr Ala Arg Asn Arg Pro Pro Phe Gly Gln Gly

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340

345

tat acc caa cct gga cct ggt tat cga taaggaggct cctctacacc 1104

Tyr Thr Gln Pro Gly Pro Gly Tyr Arg

350

355

aattaatgta gctgctagct attggcctcc caaaagactc cagtactatt ttaatttgta 1164

ttgaagaagt tcagaaattt aaaagcagag cattttttat gatatacttg ttggtgttaa 1224

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cttgactttc tagcttcctt tgtccggagg atattaaaat gctagggatga ggtttagcca 1404

tcttacttgg ctttttacta ttaacatgat gtactaaagt agagcccttt gagaatacaa 1464

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<211> 396

<212> PRT

<213> Homo sapiens

<400> 139

Met Asn Gly Gln Leu Asp Leu Ser Gly Lys Leu Ile Val Lys Ala Gln

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20 25 30

Tyr Asp Glu Leu Val Leu Met Met Gln Arg Val Phe Arg Gly Lys Leu

35 40 45

Leu Ser Asn Asp Glu Val Thr Ile Lys Tyr Lys Asp Glu Asp Gly Asp

50 55 60

Leu Ile Thr Ile Phe Asp Ser Ser Asp Leu Ser Phe Ala Ile Gln Cys

65 70 75 80

Ser Arg Ile Leu Lys Leu Thr Leu Phe Val Asn Gly Gln Pro Arg Pro

85

90

95

Leu Glu Ser Ser Gln Val Lys Tyr Leu Arg Arg Glu Leu Ile Glu Leu

100

105

110

Arg Asn Lys Val Asn Arg Leu Leu Asp Ser Leu Glu Pro Pro Gly Glu

115

120

125

Pro Gly Pro Ser Thr Asn Ile Pro Glu Asn Asp Thr Val Asp Gly Arg

130

135

140

Glu Glu Lys Ser Ala Ser Asp Ser Ser Gly Lys Gln Ser Thr Gln Val

145

150

155

160

Met Ala Ala Ser Met Ser Ala Phe Asp Pro Leu Lys Asn Gln Asp Glu

165

170

175

Ile Asn Lys Asn Val Met Ser Ala Phe Gly Leu Thr Asp Asp Gln Val

180

185

190

Ser Gly Pro Pro Ser Ala Pro Ala Glu Asp Arg Ser Gly Thr Pro Asp

195

200

205

Ser Ile Ala Ser Ser Ser Ser Ala Ala His Pro Pro Gly Val Gln Pro

210

215

220

Gln Gln Pro Pro Tyr Thr Gly Ala Gln Thr Gln Ala Gly Gln Met Tyr

225

230

235

240

Gln Gln Tyr Gln Gln Gln Ala Gly Tyr Gly Ala Gln Gln Pro Gln Ala
245 250 255

Pro Pro Gln Gln Pro Gln Gln Tyr Gly Ile Gln Tyr Ser Ala Ser Tyr
260 265 270

Ser Gln Gln Thr Gly Pro Gln Gln Pro Gln Gln Phe Gln Gly Tyr Gly
275 280 285

Gln Gln Pro Thr Ser Gln Ala Pro Ala Pro Ala Phe Ser Gly Gln Pro
290 295 300

Gln Gln Leu Pro Ala Gln Pro Pro Gln Gln Tyr Gln Ala Ser Asn Tyr
305 310 315 320

Pro Ala Gln Thr Tyr Thr Ala Gln Thr Ser Gln Pro Thr Asn Tyr Thr
325 330 335

Val Ala Pro Ala Ser Gln Pro Gly Met Ala Pro Ser Gln Pro Gly Ala
340 345 350

Tyr Gln Pro Arg Pro Gly Phe Thr Ser Leu Pro Gly Ser Thr Met Thr
355 360 365

Pro Pro Pro Ser Gly Pro Asn Pro Tyr Ala Arg Asn Arg Pro Pro Phe
370 375 380

Gly Gln Gly Tyr Thr Gln Pro Gly Pro Gly Tyr Arg
385 390 395

<210> 140

<211> 1641

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (19).. (1206)

<400> 140

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Met Asn Gly Gln Leu Asp Leu Ser Gly Lys Leu

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atc gtc aaa gct caa ctt ggg gag gat att cgg cga att cct att cat 99

Ile Val Lys Ala Gln Leu Gly Glu Asp Ile Arg Arg Ile Pro Ile His

15

20

25

aat gaa gat att act tat gat gaa tta gtg cta atg atg caa cga gtt 147

Asn Glu Asp Ile Thr Tyr Asp Glu Leu Val Leu Met Met Gln Arg Val

30

35

40

ttc aga gga aaa ctt ctg agt aat gat gaa gla aca ata aag tat aaa 195

Phe Arg Gly Lys Leu Leu Ser Asn Asp Glu Val Thr Ile Lys Tyr Lys

45

50

55

gat gaa gat gga gat ctt ata aca att ttt gat agt tct gac ctt tcc 243

Asp Glu Asp Gly Asp Leu Ile Thr Ile Phe Asp Ser Ser Asp Leu Ser
60 65 70 75

ttt gca att cag tgc agt agg ata ctg aaa ctg aca tta ttt gtt aat 291
Phe Ala Ile Gln Cys Ser Arg Ile Leu Lys Leu Thr Leu Phe Val Asn
80 85 90

ggc cag cca aga ccc ctt gaa tca agt cag gtg aaa tat ctc cgt cga 339
Gly Gln Pro Arg Pro Leu Glu Ser Ser Gln Val Lys Tyr Leu Arg Arg
95 100 105

gaa ctg ata gaa ctt cga aat aaa gtg aat cgt tta ttg gat agc ttg 387
Glu Leu Ile Glu Leu Arg Asn Lys Val Asn Arg Leu Leu Asp Ser Leu
110 115 120

gaa cca cct gga gaa cca gga cct tcc acc aat att cct gaa aat gat 435
Glu Pro Pro Gly Glu Pro Gly Pro Ser Thr Asn Ile Pro Glu Asn Asp
125 130 135

act glg gat ggt agg gaa gaa aag tct gct tct gat tct tct gga aaa 483
Thr Val Asp Gly Arg Glu Glu Lys Ser Ala Ser Asp Ser Ser Gly Lys
140 145 150 155

cag tct act cag gtt atg gca gca agt atg tct gct ttt gat cct tta 531
Gln Ser Thr Gln Val Met Ala Ala Ser Met Ser Ala Phe Asp Pro Leu
160 165 170

aaa aac caa gat gaa atc aat aaa aat gtt atg tca gcg ttt ggc tta 579
Lys Asn Gln Asp Glu Ile Asn Lys Asn Val Met Ser Ala Phe Gly Leu

175

180

185

aca gat gat cag gtt tca ggg cca ccc agt gct cct gca gaa gat cgt 627

Thr Asp Asp Gln Val Ser Gly Pro Pro Ser Ala Pro Ala Glu Asp Arg

190

195

200

tca gga aca ccc gac agc att gct tcc tcc tcc tca gca gct cac cca 675

Ser Gly Thr Pro Asp Ser Ile Ala Ser Ser Ser Ser Ala Ala His Pro

205

210

215

cca ggc gtt cag cca cag cag cca cca tat aca gga gct cag act caa 723

Pro Gly Val Gln Pro Gln Gln Pro Pro Tyr Thr Gly Ala Gln Thr Gln

220

225

230

235

gca ggt cag atg tac caa cag tac cag caa cag gcc ggc tat ggt gca 771

Ala Gly Gln Met Tyr Gln Gln Tyr Gln Gln Gln Ala Gly Tyr Gly Ala

240

245

250

cag cag ccg cag gct cca cct cag cag cct caa cag tat ggt att cag 819

Gln Gln Pro Gln Ala Pro Pro Gln Gln Pro Gln Gln Tyr Gly Ile Gln

255

260

265

tat tca gca agc tat agt cag cag act gga ccc caa caa cct cag cag 867

Tyr Ser Ala Ser Tyr Ser Gln Gln Thr Gly Pro Gln Gln Pro Gln Gln

270

275

280

ttc cag gga tat ggc cag caa cca act tcc cag gca cca gct cct gcc 915

Phe Gln Gly Tyr Gly Gln Gln Pro Thr Ser Gln Ala Pro Ala Pro Ala

285

290

295

ttt tct ggt cag cct caa caa ctg cct gct cag ccg cca cag cag tac 963

Phe Ser Gly Gln Pro Gln Gln Leu Pro Ala Gln Pro Pro Gln Gln Tyr

300 305 310 315

cag gcg agc aat tat cct gca caa act tac act gcc caa act tct cag 1011

Gln Ala Ser Asn Tyr Pro Ala Gln Thr Tyr Thr Ala Gln Thr Ser Gln

320 325 330

cct act aat tat act gtg gct cct gcc tct caa cct gga atg gct cca 1059

Pro Thr Asn Tyr Thr Val Ala Pro Ala Ser Gln Pro Gly Met Ala Pro

335 340 345

agc caa cct ggg gcc tat caa cca aga cca ggt ttt act tca ctt cct 1107

Ser Gln Pro Gly Ala Tyr Gln Pro Arg Pro Gly Phe Thr Ser Leu Pro

350 355 360

gga agt acc atg acc cct cct cca agt ggg cct aat cct tat gcg cgt 1155

Gly Ser Thr Met Thr Pro Pro Pro Ser Gly Pro Asn Pro Tyr Ala Arg

365 370 375

aac cgt cct ccc ttt ggt cag gcc tat acc caa cct gga cct ggt tat 1203

Asn Arg Pro Pro Phe Gly Gln Gly Tyr Thr Gln Pro Gly Pro Gly Tyr

380 385 390 395

cga taaggaggct cctctacacc aattaatgta gctgctagct attggcctcc 1256

Arg

caaaagactc cagtactatt ttaatttgta ttgaagaagt tcagaaattt aaaagcagag 1316

cattttttat gatatcattg ttgggtgtaa ttgaaagtat aatttgctgg aacacaaaga 1376

ccaaaatgaa agttttttcc tccctgctta aaaatgtagc agcttcttag ttactttgga 1436

acactactct tacatgtata aagtgattga ctigactttc tagcttccct tgtccggagg 1496

atattaaaat gctagggatga ggtttagcca tcttacttgg ctttttacta ttaacatgat 1556

gtactaaagt agagcccttt gagaatacaa gatattatgt ataaaatgta acactgatga 1616

taggttaata aagaigattg aatcc 1641

<210> 141

<211> 323

<212> PRT

<213> Homo sapiens

<400> 141

Met Ala Phe Ser Gly Ser Gln Ala Pro Tyr Leu Ser Pro Ala Val Pro

1

5

10

15

Phe Ser Gly Thr Ile Gln Gly Gly Leu Gln Asp Gly Leu Gln Ile Thr

20

25

30

Val Asn Gly Thr Val Leu Ser Ser Ser Gly Thr Arg Phe Ala Val Asn

35

40

45

Phe Gln Thr Gly Phe Ser Gly Asn Asp Ile Ala Phe His Phe Asn Pro
50 55 60

Arg Phe Glu Asp Gly Gly Tyr Val Val Cys Asn Thr Arg Gln Asn Gly
65 70 75 80

Ser Trp Gly Pro Glu Glu Arg Lys Thr His Met Pro Phe Gln Lys Gly
85 90 95

Met Pro Phe Asp Leu Cys Phe Leu Val Gln Ser Ser Asp Phe Lys Val
100 105 110

Met Val Asn Gly Ile Leu Phe Val Gln Tyr Phe His Arg Val Pro Phe
115 120 125

His Arg Val Asp Thr Ile Ser Val Asn Gly Ser Val Gln Leu Ser Tyr
130 135 140

Ile Ser Phe Gln Pro Pro Gly Val Trp Pro Ala Asn Pro Ala Pro Ile
145 150 155 160

Thr Gln Thr Val Ile His Thr Val Gln Ser Ala Pro Gly Gln Met Phe
165 170 175

Ser Thr Pro Ala Ile Pro Pro Met Met Tyr Pro His Pro Ala Tyr Pro
180 185 190

Met Pro Phe Ile Thr Thr Ile Leu Gly Gly Leu Tyr Pro Ser Lys Ser
195 200 205

Ile Leu Leu Ser Gly Thr Val Leu Pro Ser Ala Gln Arg Phe His Ile

210

215

220

Asn Leu Cys Ser Gly Asn His Ile Ala Phe His Leu Asn Pro Arg Phe

225

230

235

240

Asp Glu Asn Ala Val Val Arg Asn Thr Gln Ile Asp Asn Ser Trp Gly

245

250

255

Ser Glu Glu Arg Ser Leu Pro Arg Lys Met Pro Phe Val Arg Gly Gln

260

265

270

Ser Phe Ser Val Trp Ile Leu Cys Glu Ala His Cys Leu Lys Val Ala

275

280

285

Val Asp Gly Gln His Leu Phe Glu Tyr Tyr His Arg Leu Arg Asn Leu

290

295

300

Pro Thr Ile Asn Arg Leu Glu Val Gly Gly Asp Ile Gln Leu Thr His

305

310

315

320

Val Gln Thr

<210> 142

<211> 1616

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (72).. (1040)

<400> 142

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gcggcggaga g atg gcc ttc agc ggt tcc cag gct ccc tac ctg agt cca 110

Met Ala Phe Ser Gly Ser Gln Ala Pro Tyr Leu Ser Pro

1

5

10

gct gtc ccc ttt tct ggg act att caa gga ggt ctc cag gac gga ctt 158

Ala Val Pro Phe Ser Gly Thr Ile Gln Gly Gly Leu Gln Asp Gly Leu

15

20

25

cag atc act gtc aat ggg acc gtt ctc agc tcc agt gga acc agg ttt 206

Gln Ile Thr Val Asn Gly Thr Val Leu Ser Ser Ser Gly Thr Arg Phe

30

35

40

45

gct gtg aac ttt cag act ggc ttc agt gga aat gac att gcc ttc cac 254

Ala Val Asn Phe Gln Thr Gly Phe Ser Gly Asn Asp Ile Ala Phe His

50

55

60

ttc aac cct cgg ttt gaa gat gga ggg tac gtg gtg tgc aac acg agg 302

Phe Asn Pro Arg Phe Glu Asp Gly Gly Tyr Val Val Cys Asn Thr Arg

65

70

75

cag aac gga agc tgg ggg ccc gag gag agg aag aca cac atg cct ttc 350
Gln Asn Gly Ser Trp Gly Pro Glu Glu Arg Lys Thr His Met Pro Phe

80

85

90

cag aag ggg atg ccc ttt gac ctc tgc ttc ctg gtg cag agc tca gat 398
Gln Lys Gly Met Pro Phe Asp Leu Cys Phe Leu Val Gln Ser Ser Asp

95

100

105

ttc aag gtg atg gtg aac ggg atc ctc ttc gtg cag tac ttc cac cgc 446
Phe Lys Val Met Val Asn Gly Ile Leu Phe Val Gln Tyr Phe His Arg

110

115

120

125

gtg ccc ttc cac cgt gtg gac acc atc tcc gtc aat ggc tct gtg cag 494
Val Pro Phe His Arg Val Asp Thr Ile Ser Val Asn Gly Ser Val Gln

130

135

140

ctg tcc tac atc agc ttc cag cct ccc ggc gtg tgg cct gcc aac ccg 542
Leu Ser Tyr Ile Ser Phe Gln Pro Pro Gly Val Trp Pro Ala Asn Pro

145

150

155

gct ccc att acc cag aca gtc atc cac aca gtg cag agc gcc cct gga 590
Ala Pro Ile Thr Gln Thr Val Ile His Thr Val Gln Ser Ala Pro Gly

160

165

170

cag atg ttc tct act ccc gcc atc cca cct atg atg tac ccc cac ccc 638
Gln Met Phe Ser Thr Pro Ala Ile Pro Pro Met Met Tyr Pro His Pro

175

180

185

gcc tat ccg atg cct ttc atc acc acc att ctg gga ggg ctg tac cca 686

Ala Tyr Pro Met Pro Phe Ile Thr Thr Ile Leu Gly Gly Leu Tyr Pro
 190 195 200 205

tcc aag tcc atc ctc ctg tca ggc act gtc ctg ccc agt gct cag agg 734
 Ser Lys Ser Ile Leu Leu Ser Gly Thr Val Leu Pro Ser Ala Gln Arg
 210 215 220

ttc cac atc aac ctg tgc tct ggg aac cac atc gcc ttc cac ctg aac 782
 Phe His Ile Asn Leu Cys Ser Gly Asn His Ile Ala Phe His Leu Asn
 225 230 235

ccc cgt ttt gat gag aat gct gtg gtc cgc aac acc cag atc gac aac 830
 Pro Arg Phe Asp Glu Asn Ala Val Val Arg Asn Thr Gln Ile Asp Asn
 240 245 250

tcc tgg ggg tct gag gag cga agt ctg ccc cga aaa atg ccc ttc gtc 878
 Ser Trp Gly Ser Glu Glu Arg Ser Leu Pro Arg Lys Met Pro Phe Val
 255 260 265

cgt ggc cag agc ttc tca gtg tgg atc ttg tgt gaa gct cac tgc ctc 926
 Arg Gly Gln Ser Phe Ser Val Trp Ile Leu Cys Glu Ala His Cys Leu
 270 275 280 285

aag gtg gcc gtg gat ggt cag cac ctg ttt gaa tac tac cat cgc ctg 974
 Lys Val Ala Val Asp Gly Gln His Leu Phe Glu Tyr Tyr His Arg Leu
 290 295 300

agg aac ctg ccc acc atc aac aga ctg gaa gtg ggg ggc gac atc cag 1022
 Arg Asn Leu Pro Thr Ile Asn Arg Leu Glu Val Gly Gly Asp Ile Gln

305

310

315

ctg acc cat gtg cag aca taggcggctt cctggccctg gggccggggg 1070

Leu Thr His Val Gln Thr

320

ctgggggtgtg gggcagtctg ggctccttca tcateccac tteccaggcc cagccttcc 1130

aacctgcct gggatctggg cttaaatgca gaggccatgt ccttgtctgg tctgtctct 1190

ggctacagcc accttggaac ggagaaggca gctgacggg atigccttcc tcagccgcag 1250

cagcacctgg ggctccagct gctggaatcc taccatcca ggaggcaggc acagccaggg 1310

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gcagctccac cccagtccta agccaccagc tgtctgtctc tggtagggagg tggcctcctc 1430

agccctcct cctgacctt taacctcact ctcacctgc accgtgcacc aaccttcac 1490

ccctcctgga aagcaggcct gatggcttcc cactggcctc caccacctga ccagagtgtt 1550

ctcttcagag gactggctcc ttccccagtg tccttaaaat aaagaaatga aaatgcttgt 1610

tggcac 1616

<210> 143

<211> 136

<212> PRT

<213> Homo sapiens

<400> 143

Met Ala Gly Ala Ile Ile Glu Asn Met Ser Thr Lys Lys Leu Cys Ile

1 5 10 15

Val Gly Gly Ile Leu Leu Val Phe Gln Ile Ile Ala Phe Leu Val Gly

20 25 30

Gly Leu Ile Ala Pro Gly Pro Thr Thr Ala Val Ser Tyr Met Ser Val

35 40 45

Lys Cys Val Asp Ala Arg Lys Asn His His Lys Thr Lys Trp Phe Val

50 55 60

Pro Trp Gly Pro Asn His Cys Asp Lys Ile Arg Asp Ile Glu Glu Ala

65 70 75 80

Ile Pro Arg Glu Ile Glu Ala Asn Asp Ile Val Phe Ser Val His Ile

85 90 95

Pro Leu Pro His Met Ala Leu Ser Cys Gly Phe Leu Asp Gln Arg His

100 105 110

Gly His Leu Ser Val Cys Leu Leu Thr Val Ala Phe Gly Gly Arg Phe

115 120 125

Leu Gln Pro Leu Met His Cys Val

130

135

<210> 144

<211> 1252

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (225).. (632)

<400> 144

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ggcgcccttc gtcgggtcc catctcgcc gcgtccagc acctctgaag tttgcagcg 120

cccagaaagg aggcgaggaa ggagggagtg tgtgagagga gggagcaaaa agctcacctt 180

aaaacattta tttcaaggag aaaagaaaaa gggggggcgc aaaa atg gct ggg gca 236

Met Ala Gly Ala

1

att ata gaa aac atg agc acc aag aag ctg tgc att gtt ggt ggg att 284

Ile Ile Glu Asn Met Ser Thr Lys Lys Leu Cys Ile Val Gly Gly Ile

5

10

15

20

ctg ctg gtg ttc caa atc atc gcc ttt ctg glg gga ggc ttg att gct 332

Leu Leu Val Phe Gln Ile Ile Ala Phe Leu Val Gly Gly Leu Ile Ala

25

30

35

cca ggg ccc aca acg gca gtg tcc tac atg tgg gtg aaa tgt gtg gat 380

Pro Gly Pro Thr Thr Ala Val Ser Tyr Met Ser Val Lys Cys Val Asp

40

45

50

gcc cgt aag aac cat cac aag aca aaa tgg ttc gtg cct tgg gga ccc 428

Ala Arg Lys Asn His His Lys Thr Lys Trp Phe Val Pro Trp Gly Pro

55

60

65

aat cat tgt gac aag atc cga gac att gaa gag gca att cca agg gaa 476

Asn His Cys Asp Lys Ile Arg Asp Ile Glu Glu Ala Ile Pro Arg Glu

70

75

80

att gaa gcc aat gac atc gtg ttt tct gtt cac att ccc ctc ccc cac 524

Ile Glu Ala Asn Asp Ile Val Phe Ser Val His Ile Pro Leu Pro His

85

90

95

100

atg gct ctt agc tgt ggt ttc ttg gac cag cgg cat gga cat ttg tca 572

Met Ala Leu Ser Cys Gly Phe Leu Asp Gln Arg His Gly His Leu Ser

105

110

115

gtt tgc ctt ctg acg gta gct ttt gga gga aga ttc ctg cag cca cta 620

Val Cys Leu Leu Thr Val Ala Phe Gly Gly Arg Phe Leu Gln Pro Leu

120

125

130

atg cat tgt gta tgataacaaa aactctggta tgacacattt tctgtgatca 672

Met His Cys Val

135

tigttaatta gtgacatagt aacatctgta gcagctgggt agtaaacctc atgtgggggt 732
ggggtggggg tgtattcctt ggggatggt ttgggccgaa tggggagtgg aatatttgac 792
atttttcctg ttttaaattc taggatagat tttaacatcc ttgcgggtcc cagtccaagg 852
taggctgggt tcatagtcct ctcactccta atccatgacc actgtttttt tectatttat 912
atcaccaggt agcctactga gttaatattt aagttgtcaa tagataagtg tccctgtttt 972
gtggcataat ataactgaat ttcattgagaa gatttattcc accaggggia tticagcttt 1032
gaaaccaaat ctgtgtatct aatactaacc aatctgttgg atgtgggttt taaaaaatgt 1092
ttgctaaact acccaagtaa gatttactgt attaaatggc cttegggtct gaaaagcttt 1152
tttaacctct tgcttaaaat gcgttttatt ttgataagat acttcaaata gcctccaaaa 1212
gtgtagatcc aatcacttaa ataaacctgt atgtatatgc 1252

<210> 145

<211> 468

<212> PRT

<213> Homo sapiens

<400> 145

Met Pro Val Arg Thr Ile Thr Arg Gln Asn Gly Ser Cys Leu Gly Asp

1	5	10	15
Pro Ile Ile Val Thr Arg Ser Glu Thr Leu Lys Arg Gln Phe Gln Phe			
20	25	30	
Met Leu Phe Ile Leu Gln Leu Asp Ile Ala Phe Lys Leu Asn Asn Gln			
35	40	45	
Ile Arg Glu Asn Ala Glu Val Ser Met Asp Val Ser Leu Ala Tyr Arg			
50	55	60	
Asp Asp Ala Phe Ala Glu Trp Thr Glu Met Ala His Glu Arg Val Pro			
65	70	75	80
Arg Lys Leu Lys Cys Thr Phe Thr Ser Pro Lys Thr Pro Glu His Glu			
85	90	95	
Gly Arg Tyr Tyr Glu Cys Asp Val Leu Pro Phe Met Glu Ile Gly Ser			
100	105	110	
Val Ala His Lys Phe Tyr Leu Leu Asn Ile Arg Leu Pro Val Asn Glu			
115	120	125	
Lys Lys Lys Ile Asn Val Gly Ile Gly Glu Ile Lys Asp Ile Arg Leu			
130	135	140	
Val Gly Ile His Gln Asn Gly Gly Phe Thr Lys Val Trp Phe Ala Met			
145	150	155	160

Lys Thr Phe Leu Thr Pro Ser Ile Phe Ile Ile Met Val Trp Tyr Trp

165

170

175

Arg Arg Ile Thr Met Met Ser Arg Pro Pro Val Leu Leu Glu Lys Val

180

185

190

Ile Phe Ala Leu Gly Ile Ser Met Thr Phe Ile Asn Ile Pro Val Glu

195

200

205

Trp Phe Ser Ile Gly Phe Asp Trp Thr Trp Met Leu Leu Phe Gly Asp

210

215

220

Ile Arg Gln Gly Ile Phe Tyr Ala Met Leu Leu Ser Phe Trp Ile Ile

225

230

235

240

Phe Cys Gly Glu His Met Met Asp Gln His Glu Arg Asn His Ile Ala

245

250

255

Gly Tyr Trp Lys Gln Val Gly Pro Ile Ala Val Gly Ser Phe Cys Leu

260

265

270

Phe Ile Phe Asp Met Cys Glu Arg Gly Val Gln Leu Thr Asn Pro Phe

275

280

285

Tyr Ser Ile Trp Thr Thr Asp Ile Gly Thr Glu Leu Ala Met Ala Phe

290

295

300

Ile Ile Val Ala Gly Ile Cys Leu Cys Leu Tyr Phe Leu Phe Leu Cys

305

310

315

320

Phe Met Val Phe Gln Val Phe Arg Asn Ile Ser Gly Lys Gln Ser Ser

325

330

335

Leu Pro Ala Met Ser Lys Val Arg Arg Leu His Tyr Glu Gly Leu Ile

340

345

350

Phe Arg Phe Lys Phe Leu Met Leu Ile Thr Leu Ala Cys Ala Ala Met

355

360

365

Thr Val Ile Phe Phe Ile Val Ser Gln Val Thr Glu Gly His Trp Lys

370

375

380

Trp Gly Gly Val Thr Val Gln Val Asn Ser Ala Phe Phe Thr Gly Ile

385

390

395

400

Tyr Gly Met Trp Asn Leu Tyr Val Phe Ala Leu Met Phe Leu Tyr Ala

405

410

415

Pro Ser His Lys Asn Tyr Gly Glu Asp Gln Ser Asn Gly Met Gln Leu

420

425

430

Pro Cys Lys Ser Arg Glu Asp Cys Ala Leu Phe Val Ser Glu Leu Tyr

435

440

445

Gln Glu Leu Phe Ser Ala Ser Lys Tyr Ser Phe Ile Asn Asp Asn Ala

450

455

460

Ala Ser Gly Ile

465

<210> 146

<211> 1943

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (379).. (1782)

<400> 146

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ggcgccctcc gtcccggtcc catcctcgcc gcgctccagc acctctgaag ttttgcagcg 120

cccagaaaagg aggcgaggaa ggaggagtg tgtgagagga gggagcaaaa agctcacct 180

aaaacattta tttcaaggag aaaagaaaaa gggggggcgc aaaaatggct ggggcaatta 240

tagaaaacat gagcaccaag aagctgtgca ttgttggtgg gattctgctc gtgttccaaa 300

tcatgcctt tctggtggga ggcttgattg ctccagggcc cacaacggca gtgtcctaca 360

tgicggtgaa atgtgtgg atg ccc gta aga acc atc aca aga caa aat ggt 411

Met Pro Val Arg Thr Ile Thr Arg Gln Asn Gly

1

5

10

tgc tgc ctt ggg gac cca atc att gtg aca aga tcc gag aca ttg aag 459
 Ser Cys Leu Gly Asp Pro Ile Ile Val Thr Arg Ser Glu Thr Leu Lys

15

20

25

agg caa ttc caa ttc atg ctg ttt atc ctg cag ctg gac att gcc ttc 507
 Arg Gln Phe Gln Phe Met Leu Phe Ile Leu Gln Leu Asp Ile Ala Phe

30

35

40

aag cta aac aac caa atc aga gaa aat gca gaa gtc tcc atg gac gtt 555
 Lys Leu Asn Asn Gln Ile Arg Glu Asn Ala Glu Val Ser Met Asp Val

45

50

55

tcc ctg gct tac cgt gat gac gcg ttt gct gag tgg act gaa atg gcc 603
 Ser Leu Ala Tyr Arg Asp Asp Ala Phe Ala Glu Trp Thr Glu Met Ala

60

65

70

75

cat gaa aga gta cca cgg aaa ctc aaa tgc acc ttc aca tct ccc aag 651
 His Glu Arg Val Pro Arg Lys Leu Lys Cys Thr Phe Thr Ser Pro Lys

80

85

90

act cca gag cat gag ggc cgt tac tat gaa tgt gat gtc ctt cct ttc 699
 Thr Pro Glu His Glu Gly Arg Tyr Tyr Glu Cys Asp Val Leu Pro Phe

95

100

105

atg gaa att ggg tct gtg gcc cat aag ttt tac ctt tta aac atc cgg 747
 Met Glu Ile Gly Ser Val Ala His Lys Phe Tyr Leu Leu Asn Ile Arg

110

115

120

ctg cct gtg aat gag aag aag aaa atc aat gtg gga att ggg gag ata 795

Leu Pro Val Asn Glu Lys Lys Lys Ile Asn Val Gly Ile Gly Glu Ile

125

130

135

aag gat atc cgg ttg gtg ggg atc cac caa aat gga ggc ttc acc aag 843

Lys Asp Ile Arg Leu Val Gly Ile His Gln Asn Gly Gly Phe Thr Lys

140

145

150

155

gtg tgg ttt gcc atg aag acc ttc ctt acg ccc agc atc ttc atc att 891

Val Trp Phe Ala Met Lys Thr Phe Leu Thr Pro Ser Ile Phe Ile Ile

160

165

170

atg gtg tgg tat tgg agg agg atc acc atg atg tcc cga ccc cca gtg 939

Met Val Trp Tyr Trp Arg Arg Ile Thr Met Met Ser Arg Pro Pro Val

175

180

185

ctt ctg gaa aaa gtc atc ttt gcc ctt ggg att tcc atg acc ttt atc 987

Leu Leu Glu Lys Val Ile Phe Ala Leu Gly Ile Ser Met Thr Phe Ile

190

195

200

aat atc cca gtg gaa tgg ttt tcc atc ggg ttt gac tgg acc tgg atg 1035

Asn Ile Pro Val Glu Trp Phe Ser Ile Gly Phe Asp Trp Thr Trp Met

205

210

215

ctg ctg ttt ggt gac atc cga cag ggc atc ttc tat gcg atg ctt ctg 1083

Leu Leu Phe Gly Asp Ile Arg Gln Gly Ile Phe Tyr Ala Met Leu Leu

220

225

230

235

tcc ttc tgg atc atc ttc tgt ggc gag cac atg atg gal cag cac gag 1131

Ser Phe Trp Ile Ile Phe Cys Gly Glu His Met Met Asp Gln His Glu

240	245	250	
cgg aac cac atc gca ggg tat tgg aag caa gtc gga ccc att gcc gtt			1179
Arg Asn His Ile Ala Gly Tyr Trp Lys Gln Val Gly Pro Ile Ala Val			
255	260	265	
ggc tcc ttc tgc ctc ttc ata ttt gac atg tgt gag aga ggg gta caa			1227
Gly Ser Phe Cys Leu Phe Ile Phe Asp Met Cys Glu Arg Gly Val Gln			
270	275	280	
ctc acg aat ccc ttc tac agt atc tgg act aca gac att gga aca gag			1275
Leu Thr Asn Pro Phe Tyr Ser Ile Trp Thr Thr Asp Ile Gly Thr Glu			
285	290	295	
ctg gcc atg gcc ttc atc atc gtg gct gga atc tgc ctc tgc ctc tac			1323
Leu Ala Met Ala Phe Ile Ile Val Ala Gly Ile Cys Leu Cys Leu Tyr			
300	305	310	315
ttc ctg ttt cta tgc ttc atg gta ttt cag gtg ttt cgg aac atc agt			1371
Phe Leu Phe Leu Cys Phe Met Val Phe Gln Val Phe Arg Asn Ile Ser			
320	325	330	
ggg aag cag tcc agc ctg cca gct atg agc aaa gtc cgg cgg cta cac			1419
Gly Lys Gln Ser Ser Leu Pro Ala Met Ser Lys Val Arg Arg Leu His			
335	340	345	
tat gag ggg cta att ttt agg ttc aag ttc ctc atg ctt atc acc ttg			1467
Tyr Glu Gly Leu Ile Phe Arg Phe Lys Phe Leu Met Leu Ile Thr Leu			
350	355	360	

gcc tgc gct gcc atg act gtc atc ttc ttc atc gtt agt cag gta acg 1515

Ala Cys Ala Ala Met Thr Val Ile Phe Phe Ile Val Ser Gln Val Thr

365

370

375

gaa ggc cat tgg aaa tgg ggc ggc gtc aca gtc caa gtg aac agt gcc 1563

Glu Gly His Trp Lys Trp Gly Gly Val Thr Val Gln Val Asn Ser Ala

380

385

390

395

ttt ttc aca ggc atc tat ggg atg tgg aat ctg tat gtc ttt gct ctg 1611

Phe Phe Thr Gly Ile Tyr Gly Met Trp Asn Leu Tyr Val Phe Ala Leu

400

405

410

atg ttc ttg tat gca cca tcc cat aaa aac tat gga gaa gac cag tcc 1659

Met Phe Leu Tyr Ala Pro Ser His Lys Asn Tyr Gly Glu Asp Gln Ser

415

420

425

aat gga atg caa ctc cca tgt aaa tcg agg gaa gat tgt gct ttg ttt 1707

Asn Gly Met Gln Leu Pro Cys Lys Ser Arg Glu Asp Cys Ala Leu Phe

430

435

440

gtt tcg gaa ctt tat caa gaa ttg ttc agc gct tcg aaa tat tcc ttc 1755

Val Ser Glu Leu Tyr Gln Glu Leu Phe Ser Ala Ser Lys Tyr Ser Phe

445

450

455

atc aat gac aac gca gct tct ggt att tgagtcaaca aggcaacaca 1802

Ile Asn Asp Asn Ala Ala Ser Gly Ile

460

465

tgtttatcag ctttgcattt gcagttgtca cagtcacatt gattgtactt gtatacgcac 1862

acaaatacac tcatttagcc tttatctcaa aatgttaaatt ataaggaaaa aagcgtcaac 1922

aataaatatt ctttgagtat t 1943

<210> 147

<211> 460

<212> PRT

<213> Homo sapiens

<400> 147

Met Pro Val Arg Thr Ile Thr Arg Gln Asn Gly Ser Cys Leu Gly Asp

1 5 10 15

Pro Ile Ile Val Thr Arg Ser Glu Thr Leu Lys Arg Gln Phe Gln Gly

20 25 30

Lys Leu Lys Pro Met Thr Ser Cys Phe Leu Phe Thr Phe Pro Ser Pro

35 40 45

Met Asp Val Ser Leu Ala Tyr Arg Asp Asp Ala Phe Ala Glu Trp Thr

50 55 60

Glu Met Ala His Glu Arg Val Pro Arg Lys Leu Lys Cys Thr Phe Thr

65 70 75 80

Ser Pro Lys Thr Pro Glu His Glu Gly Arg Tyr Tyr Glu Cys Asp Val

85

90

95

Leu Pro Phe Met Glu Ile Gly Ser Val Ala His Lys Phe Tyr Leu Leu

100

105

110

Asn Ile Arg Leu Pro Val Asn Glu Lys Lys Lys Ile Asn Val Gly Ile

115

120

125

Gly Glu Ile Lys Asp Ile Arg Leu Val Gly Ile His Gln Asn Gly Gly

130

135

140

Phe Thr Lys Val Trp Phe Ala Met Lys Thr Phe Leu Thr Pro Ser Ile

145

150

155

160

Phe Ile Ile Met Val Trp Tyr Trp Arg Arg Ile Thr Met Met Ser Arg

165

170

175

Pro Pro Val Leu Leu Glu Lys Val Ile Phe Ala Leu Gly Ile Ser Met

180

185

190

Thr Phe Ile Asn Ile Pro Val Glu Trp Phe Ser Ile Gly Phe Asp Trp

195

200

205

Thr Trp Met Leu Leu Phe Gly Asp Ile Arg Gln Gly Ile Phe Tyr Ala

210

215

220

Met Leu Leu Ser Phe Trp Ile Ile Phe Cys Gly Glu His Met Met Asp

225

230

235

240

Gln His Glu Arg Asn His Ile Ala Gly Tyr Trp Lys Gln Val Gly Pro
245 250 255

Ile Ala Val Gly Ser Phe Cys Leu Phe Ile Phe Asp Met Cys Glu Arg
260 265 270

Gly Val Gln Leu Thr Asn Pro Phe Tyr Ser Ile Trp Thr Thr Asp Ile
275 280 285

Gly Thr Glu Leu Ala Met Ala Phe Ile Ile Val Ala Gly Ile Cys Leu
290 295 300

Cys Leu Tyr Phe Leu Phe Leu Cys Phe Met Val Phe Gln Val Phe Arg
305 310 315 320

Asn Ile Ser Gly Lys Gln Ser Ser Leu Pro Ala Met Ser Lys Val Arg
325 330 335

Arg Leu His Tyr Glu Gly Leu Ile Phe Arg Phe Lys Phe Leu Met Leu
340 345 350

Ile Thr Leu Ala Cys Ala Ala Met Thr Val Ile Phe Phe Ile Val Ser
355 360 365

Gln Val Thr Glu Gly His Trp Lys Trp Gly Gly Ile Thr Val Gln Val
370 375 380

Asn Ser Ala Phe Phe Thr Gly Ile Tyr Gly Met Trp Asn Leu Tyr Val
385 390 395 400

Phe Ala Leu Met Phe Leu Tyr Ala Pro Ser His Lys Asn Tyr Gly Glu
405 410 415

Asp Gln Ser Asn Gly Met Gln Leu Pro Cys Lys Ser Arg Glu Asp Cys
420 425 430

Ala Leu Phe Val Ser Glu Leu Tyr Gln Glu Leu Phe Ser Ala Ser Lys
435 440 445

Tyr Ser Phe Ile Asn Asp Asn Ala Ala Ser Gly Ile
450 455 460

<210> 148

<211> 1919

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (376).. (1755)

<400> 148

atcacagctc cgggcattgg gggaaccgga gccggctgcg cggggggaat ccgtgcgggc 60

gccttcgctc ccggtcccat cctcgccgcg ctccagcacc tctgaagttt tgcagcgccc 120

agaaaggagg cgaggaagga gggagtgtat gagaggagg agcaaaaagc tcaccctaaa 180

acatttatit caaggagaaa agaaaaaggg gggcgcaaa aatggctggg gcaattatag 240

aaaacatgag caccaagaag ctgtgcattg ttggtgggat tctgctcgtg ttccaaatca 300

tcgccittct ggtgggaggc ttgattgcic cagggccac aacggcagtg tcctacatgt 360

cggtgaaatg tgtgg atg ccc gta aga acc atc aca aga caa aat ggt tgc 411

Met Pro Val Arg Thr Ile Thr Arg Gln Asn Gly Ser

1

5

10

tgc ctt ggg gac cca atc att gtg aca aga tcc gag aca ttg aag agg 459

Cys Leu Gly Asp Pro Ile Ile Val Thr Arg Ser Glu Thr Leu Lys Arg

15

20

25

caa ttc caa ggg aaa ttg aag cca atg aca tgc tgt ttt ctg ttc aca 507

Gln Phe Gln Gly Lys Leu Lys Pro Met Thr Ser Cys Phe Leu Phe Thr

30

35

40

ttc ccc tcc ccc atg gac gtt tcc ctg gct tac cgt gat gac gcg ttt 555

Phe Pro Ser Pro Met Asp Val Ser Leu Ala Tyr Arg Asp Asp Ala Phe

45

50

55

60

gct gag tgg act gaa atg gcc cat gaa aga gta cca cgg aaa ctc aaa 603

Ala Glu Trp Thr Glu Met Ala His Glu Arg Val Pro Arg Lys Leu Lys

65

70

75

tgc acc ttc aca tct ccc aag act cca gag cat gag ggc cgt tac tat 651

Cys Thr Phe Thr Ser Pro Lys Thr Pro Glu His Glu Gly Arg Tyr Tyr

80

85

90

gaa tgt gat gtc ctt cct ttc atg gaa att ggg tct gtg gcc cat aag 699

Glu Cys Asp Val Leu Pro Phe Met Glu Ile Gly Ser Val Ala His Lys

95

100

105

ttt tac ctt tta aac atc cgg ctg cct gtg aat gag aag aag aaa atc 747

Phe Tyr Leu Leu Asn Ile Arg Leu Pro Val Asn Glu Lys Lys Lys Ile

110

115

120

aat gtg gga att ggg gag ata aag gat atc cgg ttg gtg ggg atc cac 795

Asn Val Gly Ile Gly Glu Ile Lys Asp Ile Arg Leu Val Gly Ile His

125

130

135

140

caa aat gga ggc ttc acc aag gtg tgg ttt gcc atg aag acc ttc ctt 843

Gln Asn Gly Gly Phe Thr Lys Val Trp Phe Ala Met Lys Thr Phe Leu

145

150

155

acg ccc agc atc ttc atc att atg gtg tgg tat tgg agg agg atc acc 891

Thr Pro Ser Ile Phe Ile Ile Met Val Trp Tyr Trp Arg Arg Ile Thr

160

165

170

atg atg tcc cga ccc cca gtg ctt ctg gaa aaa gtc atc ttt gcc ctt 939

Met Met Ser Arg Pro Pro Val Leu Leu Glu Lys Val Ile Phe Ala Leu

175

180

185

ggg att tcc atg acc ttt atc aat atc cca gtg gaa tgg ttt tcc atc 987

Gly Ile Ser Met Thr Phe Ile Asn Ile Pro Val Glu Trp Phe Ser Ile

190

195

200

ggg ttt gac tgg acc tgg atg ctg ctg ttt ggt gac atc cga cag ggc 1035
Gly Phe Asp Trp Thr Trp Met Leu Leu Phe Gly Asp Ile Arg Gln Gly
205 210 215 220

atc ttc tat gcg atg ctt ctg tcc ttc tgg atc atc ttc tgt ggc gag 1083
Ile Phe Tyr Ala Met Leu Leu Ser Phe Trp Ile Ile Phe Cys Gly Glu
225 230 235

cac atg atg gat cag cac gag cgg aac cac atc gca ggg tat tgg aag 1131
His Met Met Asp Gln His Glu Arg Asn His Ile Ala Gly Tyr Trp Lys
240 245 250

caa gtc gga ccc att gcc gtt ggc tcc ttc tgc ctc ttc ata ttt gac 1179
Gln Val Gly Pro Ile Ala Val Gly Ser Phe Cys Leu Phe Ile Phe Asp
255 260 265

atg tgt gag aga ggg gta caa ctc acg aat ccc ttc tac agt atc tgg 1227
Met Cys Glu Arg Gly Val Gln Leu Thr Asn Pro Phe Tyr Ser Ile Trp
270 275 280

act aca gac att gga aca gag ctg gcc atg gcc ttc atc atc gtg gct 1275
Thr Thr Asp Ile Gly Thr Glu Leu Ala Met Ala Phe Ile Ile Val Ala
285 290 295 300

gga atc tgc ctc tgc ctc tac ttc ctg ttt cta tgc ttc atg gta ttt 1323
Gly Ile Cys Leu Cys Leu Tyr Phe Leu Phe Leu Cys Phe Met Val Phe
305 310 315

cag gtg ttt cgg aac atc agt ggg aag cag tcc agc ctg cca gct atg 1371
Gln Val Phe Arg Asn Ile Ser Gly Lys Gln Ser Ser Leu Pro Ala Met

320

325

330

agc aaa gtc cgg cgg cta cac tat gag ggg cta att ttt agg ttc aag 1419
Ser Lys Val Arg Arg Leu His Tyr Glu Gly Leu Ile Phe Arg Phe Lys

335

340

345

ttc ctc atg ctt atc acc ttg gcc tgc gct gcc atg act gtc atc ttc 1467
Phe Leu Met Leu Ile Thr Leu Ala Cys Ala Ala Met Thr Val Ile Phe

350

355

360

ttc atc gtt agt cag gta acg gaa ggc cat tgg aaa tgg ggc ggc atc 1515
Phe Ile Val Ser Gln Val Thr Glu Gly His Trp Lys Trp Gly Gly Ile

365

370

375

380

aca gtc caa gtg aac agt gcc ttt ttc aca ggc atc tat ggg atg tgg 1563
Thr Val Gln Val Asn Ser Ala Phe Phe Thr Gly Ile Tyr Gly Met Trp

385

390

395

aat ctg tat gtc ttt gct ctg atg ttc ttg tat gca cca tcc cat aaa 1611
Asn Leu Tyr Val Phe Ala Leu Met Phe Leu Tyr Ala Pro Ser His Lys

400

405

410

aac tat gga gaa gac cag tcc aat gga atg caa ctc cca tgt aaa tcg 1659
Asn Tyr Gly Glu Asp Gln Ser Asn Gly Met Gln Leu Pro Cys Lys Ser

415

420

425

agg gaa gat tgt gct ttg ttt gtt tcg gaa ctt tat caa gaa ttg ttc 1707

Arg Glu Asp Cys Ala Leu Phe Val Ser Glu Leu Tyr Gln Glu Leu Phe

430

435

440

agc gct tgc aaa tat tcc ttc atc aat gac aac gca gct tct ggt att 1755

Ser Ala Ser Lys Tyr Ser Phe Ile Asn Asp Asn Ala Ala Ser Gly Ile

445

450

455

460

tgagtcacaa aggcaacaca tgtttatcag ctttgcattt gcagttgtca cagtcacatt 1815

gattgtactt gtatcgcac acaaatacac tcatttagcc tttatctcaa aatgitaat 1875

ataaggaaaa aagcgtcaac aataaatatt ctttgagtat tgic 1919

<210> 149

<211> 183

<212> PRT

<213> Homo sapiens

<400> 149

Met Lys Leu Leu Ser Leu Val Ala Val Val Gly Cys Leu Leu Val Pro

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Pro Ala Glu Ala Asn Lys Ser Ser Glu Asp Ile Arg Cys Lys Cys Ile

20

25

30

Cys Pro Pro Tyr Arg Asn Ile Ser Gly His Ile Tyr Asn Gln Asn Val

35

40

45

Ser Gln Lys Asp Cys Asn Cys Leu His Val Val Glu Pro Met Pro Val

50

55

60

Pro Gly His Asp Val Glu Ala Tyr Cys Leu Leu Cys Glu Cys Arg Tyr

65

70

75

80

Glu Glu Arg Ser Thr Thr Thr Ile Lys Val Ile Ile Val Ile Tyr Leu

85

90

95

Ser Val Val Gly Ala Leu Leu Leu Tyr Met Ala Phe Leu Met Leu Val

100

105

110

Asp Pro Leu Ile Arg Lys Pro Asp Ala Tyr Thr Glu Gln Leu His Asn

115

120

125

Glu Glu Glu Asn Glu Asp Ala Arg Ser Met Ala Ala Ala Ala Ser

130

135

140

Leu Gly Gly Pro Arg Ala Asn Thr Val Leu Glu Arg Val Glu Gly Ala

145

150

155

160

Gln Gln Arg Trp Lys Leu Gln Val Gln Glu Gln Arg Lys Thr Val Phe

165

170

175

Asp Arg His Lys Met Leu Ser

180

<210> 150

<211> 1562

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (120).. (668)

<400> 150

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ttgcggctgc agcgggcttg taggtgtccg gctttgctgg cccagcaagc ctgataagc 119

atg aag ctc tta tct ttg gtg gct gtg gtc ggg tgt ttg ctg gtg ccc 167

Met Lys Leu Leu Ser Leu Val Ala Val Val Gly Cys Leu Leu Val Pro

1

5

10

15

cca gct gaa gcc aac aag agt tct gaa gat atc cgg tgc aaa tgc atc 215

Pro Ala Glu Ala Asn Lys Ser Ser Glu Asp Ile Arg Cys Lys Cys Ile

20

25

30

tgt cca cct tat aga aac atc agt ggg cac att tac aac cag aat gta 263

Cys Pro Pro Tyr Arg Asn Ile Ser Gly His Ile Tyr Asn Gln Asn Val

35

40

45

tcc cag aag gac tgc aac tgc ctg cac gtg gtg gag ccc atg cca gtg 311

Ser Gln Lys Asp Cys Asn Cys Leu His Val Val Glu Pro Met Pro Val

50

55

60

cct ggc cat gac gtg gag gcc tac tgc ctg ctg tgc gag tgc agg tac 359
 Pro Gly His Asp Val Glu Ala Tyr Cys Leu Leu Cys Glu Cys Arg Tyr
 65 70 75 80

gag gag cgc agc acc acc acc atc aag gtc atc att gtc atc tac ctg 407
 Glu Glu Arg Ser Thr Thr Thr Ile Lys Val Ile Ile Val Ile Tyr Leu
 85 90 95

tcc gtg gtg ggt gcc ctg ttg ctc tac atg gcc ttc ctg atg ctg gtg 455
 Ser Val Val Gly Ala Leu Leu Leu Tyr Met Ala Phe Leu Met Leu Val
 100 105 110

gac cct ctg atc cga aag ccg gat gca tat act gag caa ctg cac aat 503
 Asp Pro Leu Ile Arg Lys Pro Asp Ala Tyr Thr Glu Gln Leu His Asn
 115 120 125

gag gag gag aat gag gat gct cgc tct atg gca gca gct gct gca tcc 551
 Glu Glu Glu Asn Glu Asp Ala Arg Ser Met Ala Ala Ala Ala Ala Ser
 130 135 140

ctc ggg gga ccc cga gca aac aca gtc ctg gag cgt gtg gaa ggt gcc 599
 Leu Gly Gly Pro Arg Ala Asn Thr Val Leu Glu Arg Val Glu Gly Ala
 145 150 155 160

cag cag cgg tgg aag ctg cag gtg cag gag cag cgg aag aca gtc ttc 647
 Gln Gln Arg Trp Lys Leu Gln Val Gln Glu Gln Arg Lys Thr Val Phe
 165 170 175

gat cgg cac aag atg ctc agc tagatgggct ggtgtggttg ggtcaaggcc 698

Asp Arg His Lys Met Leu Ser

180

ccaacaccat ggcgccagc ttccaggctg gacaaagcag ggggctactt ctcccttccc 758
tcggttccag tcttcccttt aaaagcctgt ggcatitttc ctccttctcc ctaacttiag 818
aaatgttgta cttggctatt ttgattaggg aagagggatg tggctctcga tctccgttgt 878
cttcttgggt ctttgggggt gaagggaggg ggaaggcagg ccagaaggga atggagacat 938
tcgaggcggc ctcaggagtg gatggaict gtctctctg gctccactct tgccgccttc 998
cagctctgag tcttggaat gtgtttacc ttggaagata aagctgggtc ttcaggaact 1058
cagtgtctgg gaggaaagca tggcccagca ttcagcatgt gtccctttct gcagtgttc 1118
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aagctgggtg tcgctgtccc ctgtgcactt ctgcactgg ggcatggagt gcccattcat 1298
actctgtgc cggccccct accgtcactt gaggggtctg ggcagtcctt cctctcccca 1358
gtgtccacag tcactgagcc agacggctcg ttggaacatg agactcgagg ctgagcgtgg 1418
atctgaacac cacagccctt gtacttgggt tgccctttgt cctgaactt cgttgtacca 1478

gtgcatggag agaaaatttt gtcctcttgt cttagagttg tgtgtaaatc aaggaagcca 1538

tcattaaatt gttttatttc tctc 1562

<210> 151

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Primer

<400> 151

cttctgctct aaaagctgcg 20

<210> 152

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Primer

<400> 152

cgacctgcag ctgcagcaca 20

FIG.1

